

1 GGATCCCAGGGAACGTGACC ATG GTC GTA GGG ATG ACT TGA CAGTTTCAACGGGGTGCGACCACCGTTGCGC 72
 1 M V V G M T * 7

73 TCAGAAGGCATACGTTGGTGAACACGTCGGAAAGCTGGGAGGTGAATCTG ATG GCT GGC GAC CAA GAG CTG 144
 1 M A G D Q E L 7

145 GAA CTG CGG TTC GAC GTT CCT CTT TAC ACG CTT GCC GAG GCA TCG CCG TAC CTG GTG GTT 204
 8 E L R F D V P L Y T L A E A S R Y L V V 27

205 CCC CGC GCC ACC CTG GCT ACG TGG GCT GAC GGC TAC GAG CGT CCG CCG GCC AAC GCA CCG 264
 28 P R A T L A T W A D G Y E R R P A N A P 47

265 GCG GTC CAG GGG CAA CCG ATC GCC TTT GAC GCC TAT TCG GTC GCG CAG CTT TTT GGC GAC 324
 48 A V Q G Q P I A F D A Y S V A Q L F G D 67

325 GTC ACT GGT GCC CGC GTT GCG GGC GTC CAG CCG CAG CGA CAC CAC ATA CGG CCG GTC CGG 384
 68 V T G A R V A G V Q P Q R H H I R P V R 87

385 TTG CGG GGG CCG TTG GGT GGG GTT GGG TGC CTC CGT CAC CCC AGG CAG TTC GCT GGC TAT 444
 88 L R G P L G G V G C L R H P R Q F A G Y 107

445 TTG TCG CAG TAG CGCGACGGCATTGTGCG ATG TCT TGG TAG CTAGCATCCGGTCGGGGGGCCGCTACCAGCG 515
 108 L S Q * M S W * 4

516 CCAGCGCCGGGGCTCCCCGGTCCGGGTAGTGCGGTCGAGTTGGTCGTGGACCAGCA ATG ACT GCG ACC CGG 587
 1 M T A T R 5

588 CGA CTT CGA AAC CGC CAC CGG TTA GAT TCC CCG ACT GCG TCA TCG CCA GGT AAA CCG CCG 647
 6 R L R N R H R L D S P T A S S P G K P P 25

648 GCA CTA ACG CCA GCA ACC AAC CCG TGA AGACCAACCAACGGCACCTGCGCAGGTTGCGGCTCAACCGCATC 718
 26 A L T P A T N P * 34

719 ATG AAC TGC TGG ATT TCG GAC TCC CCG TAC TCT CGC GCA GTG CGT GCC CGC GAG CCT ACC 778
 1 M N C W I S D S P Y S R A V R A R E P T 20

779 GAA GAT CGC GTG CAT GCG TTC GGC GTG GAC CGC ACA GCA CCT GGA GTT GGC GGC GCC GAG 838
 21 E D R V H A F G V D R T A P G V G G A E 40

839 GGC CGA GAT GGC AGG ATG ACG GAT CGT CCG GGG CGG GAA CTC CCA GGC CGC CGG ACC GTC 898
 41 G R D G R M T D R R G R E L P G R R T V 60

899 GCA AAC CCG TCG CAA ACC CGT CGC AAA CCG TAA GGAGTCATCC ATG AAG ACA GGC ACC GCG 959
 61 A N P S Q T R R K P * M K T G T A 6

960 ACG ACG CGG CGC AGG CTG TTG GCA GTA CTG ATC GCC CTC GCG TTG CCG GGG GCC GCC GTT 1019
 7 T T R R R L L A V L I A L A L P G A A V 26

1020 GCG CTG CTG GCC GAA CCA TCA GCG ACC GGC GCG TCG GAC CCG TGC GCG GCC AGC GAA GTG 1079
 27 A L L A E P S A T G A S D P C A A S E V 46

1080 GCG AGG ACG GTC GGT TCG GTC GCC AAG TCG ATG GGC GAC TAC CTG GAT TCA CAC CCA GAG 1139
 47 A R T V G S V A K S M G D Y L D S H P E 66

1140 ACC AAC CAG GTG ATG ACC GCG GTC TTG CAG CAG CAG GTA GGG CCG GGG TCG GTC GCA TCG 1199
 67 T N Q V M T A V L Q Q Q V G P G S V A S 86

1200 CTG AAG GCC CAT TTC GAG GCG AAT CCC AAG GTC GCA TCG GAT CC 1243
 87 L K A H F E A N P K V A S D 100

SEQ ID No.1

FIGURE 1

Insert of the clone containing DP428 and contained in seq1

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1/1
GAT CGC CTT TGA CGC CTA TTC GGT CGC GCA GCT TTT TGG CGA CGT CAC TGG TGC CCG CGT
asp arg leu OPA arg leu phe gly arg ala ala phe trp arg arg his trp cys pro arg
61/21
TGC GGG CGT CCA GCC GCA GCG ACA CCA CAT ACG GCC GGT CCG GTT GCG GGG GCC GTT GGG
cys gly arg pro ala ala ala thr pro his thr ala gly pro val ala gly ala val gly
121/41
TGG GGT TGG GTG CCT CCG TCA CCC CAG GCA GTT CGC TGG CTA TTT GTC GCA GTA GCG CGA
trp gly trp val pro pro ser pro gln ala val arg trp leu phe val ala val ala arg
181/61
CGG CAT TGT CGA TGT CTT GGT AGC TAG CAT CCG GTC GGG GGG CCG CTA CCA GCG CCA GCG
arg his cys arg cys leu gly ser AMB his pro val gly gly pro leu pro ala pro ala
241/81
CCG GGG CTC CCC GGT CCG GGT AGT GCG CGT CGA GTT GGT CGT GGA CCA GCA ATG ACT GCG
pro gly leu pro gly pro gly ser ala arg arg val gly arg gly pro ala met thr ala
301/101
ACC CGG CGA CTT CGA AAC CGC CAC CGG TTA GAT TCC CCG ACT GCG TCA TCG CCA GGT AAA
thr arg arg leu arg asn arg his arg leu asp ser pro thr ala ser ser pro gly lys
361/121
CCG CCG GCA CTA ACG CCA GCA ACC AAC CCG TGA AGA CCA ACC AAC GGC ACC TGC GCA GGT
pro pro ala leu thr pro ala thr asn pro OPA arg pro thr asn gly thr cys ala gly
421/141
TGC GGC TCA ACC GCA TCA TGA ACT GCT GGA TTT CGG ACT CCC CGT ACT CTC GCG CAG TGC
cys gly ser thr ala ser OPA thr ala gly phe arg thr pro arg thr leu ala gln cys
481/161
GTG CCC GCG AGC CTA CCG AAG ATC GCG TGC ATG CGT TCG GCG TGG ACC GCA CAG CAC CTG
val pro ala ser leu pro lys ile ala cys met arg ser ala trp thr ala gln his leu
541/181
GAG TTG GCG GCG CCG AGG GCC GAG ATG GCA GGA TGA CGG ATC GTC GGG GGC GGG AAC TCC
glu leu ala ala pro arg ala glu met ala gly OPA arg ile val gly gly gly asn ser
601/201
CAG GCC GCC GGA CCG TCG CAA ACC CGT CGC AAA CCC GTC GCA AAC CGT AAG GAG TCA TCC
gln ala ala gly pro ser gln thr arg arg lys pro val ala asn arg lys glu ser ser
661/221
ATG AAG ACA GGC ACC GCG ACG ACG CGG CGC AGG CTG TTG GCA GTA CTG ATC GCC CTC GCG
met lys thr gly thr ala thr thr arg arg arg leu leu ala val leu ile ala leu ala
721/241
TTG CCG GGG GCC GCC GTT GCG CTG CTG GCC GAA CCA TCA GCG ACC GGC GCG TCG GAC CCG
leu pro gly ala ala val ala leu leu ala glu pro ser ala thr gly ala ser asp pro
781/261
TGC GCG GCC AGC GAA GTG GCG AGG ACG GTC GGT TCG GTC GCC AAG TCG ATG GGC GAC TAC
cys ala ala ser glu val ala arg thr val gly ser val ala lys ser met gly asp tyr
841/281
CTG GAT TCA CAC CCA GAG ACC AAC CAG GTG ATG ACC GCG GTC TTG CAG CAG CAG GTA GGG
leu asp ser his pro glu thr asn gln val met thr ala val leu gln gln gln val gly
901/301
CCG GGG TCG GTC GCA TCG CTG AAG GCC CAT TTC GAG GCG AAT CCC AAG GTC GCA TCG GAT C
pro gly ser val ala ser leu lys ala his phe glu ala asn pro lys val ala ser asp

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SEQ ID No.1A'

FIGURE 1A'

Insert of the clone containing DP428, other reading frame

2/1	32/11
ATC GCC TTT GAC GCC TAT TCG GTC GCG CAG CTT TTT GGC GAC GTC ACT GGT GCC CGC GTT	
ile ala phe asp ala tyr ser val ala gln leu phe gly asp val thr gly ala arg val	
62/21	92/31
GCG GGC GTC CAG CCG CAG CGA CAC CAC ATA CGG CCG GTC CCG TTG CCG GGG CCG TTG GGT	
ala gly val gln pro gln arg his his ile arg pro val arg leu arg gly pro leu gly	
122/41	152/51
GGG GTT GGG TGC CTC CGT CAC CCC AGG CAG TTC GCT GGC TAT TTG TCG CAG TAG CGC GAC	
gly val gly cys leu arg his pro arg gln phe ala gly tyr leu ser gln AMB arg asp	
182/61	212/71
GGC ATT GTC GAT GTC TTG GTA GCT AGC ATC CGG TCG GGG GGC CGC TAC CAG CGC CAG CGC	
gly ile val asp val leu val ala ser ile arg ser gly gly arg tyr gln arg gln arg	
242/81	272/91
CGG GGC TCC CCG GTC CGG GTA GTG CGC GTC GAG TTG GTC GTG GAC CAG CAA TGA CTG CGA	
arg gly ser pro val arg val val arg val glu leu val val asp gln gln OPA leu arg	
302/101	332/111
CCC GGC GAC TTC GAA ACC GCC ACC GGT TAG ATT CCC CGA CTG CGT CAT CGC CAG GTA AAC	
pro gly asp phe glu thr ala thr gly AMB ile pro arg leu arg his arg gln val asn	
362/121	392/131
CGC CGG CAC TAA CGC CAG CAA CCA ACC CGT GAA GAC CAA CCA ACG GCA CCT GCG CAG GTT	
arg arg his OCH arg gln gln pro thr arg glu asp gln pro thr ala pro ala gln val	
422/141	452/151
GCG GCT CAA CCG CAT CAT GAA CTG CTG GAT TTC GGA CTC CCC GTA CTC TCG CGC AGT GCG	
ala ala gln pro his his glu leu leu asp phe gly leu pro val leu ser arg ser ala	
482/161	512/171
TGC CCG CGA GCC TAC CGA AGA TCG CGT GCA TGC GTT CCG CGT GGA CCG CAC AGC ACC TGG	
cys pro arg ala tyr arg arg ser arg ala cys val arg arg gly pro his ser thr trp	
542/181	572/191
AGT TGG CGG CGC CGA GGG CCG AGA TGG CAG GAT GAC GGA TCG TCG GGG GCG GGA ACT CCC	
ser trp arg arg arg gly pro arg trp gln asp asp gly ser ser gly ala gly thr pro	
602/201	632/211
AGG CCG CCG GAC CGT CGC AAA CCC GTC GCA AAC CCG TCG CAA ACC GTA AGG AGT CAT CCA	
arg pro pro asp arg arg lys pro val ala asn pro ser gln thr val arg ser his pro	
662/221	692/231
TGA AGA CAG GCA CCG CGA CGA CGC GGC GCA GGC TGT TGG CAG TAC TGA TCG CCC TCG CGT	
OPA arg gln ala pro arg arg arg gly ala gly cys trp gln tyr OPA ser pro ser arg	
722/241	752/251
TGC CGG GGG CCG CCG TTG CGC TGC TGG CCG AAC CAT CAG CGA CCG GCG CGT CGG ACC CGT	
cys arg gly pro pro leu arg cys trp pro asn his gln arg pro ala arg arg thr arg	
782/261	812/271
GCG CGG CCA GCG AAG TGG CGA GGA CGG TCG GTT CGG TCG CCA AGT CGA TGG GCG ACT ACC	
ala arg pro ala lys trp arg gly arg ser val arg ser pro ser arg trp ala thr thr	
842/281	872/291
TGG ATT CAC ACC CAG AGA CCA ACC AGG TGA TGA CCG CGG TCT TGC AGC AGC AGG TAG GGC	
trp ile his thr gln arg pro thr arg OPA OPA pro arg ser cys ser ser arg AMB gly	
902/301	932/311
CGG GGT CGG TCG CAT CGC TGA AGG CCC ATT TCG AGG CGA ATC CCA AGG TCG CAT CGG ATC	
arg gly arg ser his arg OPA arg pro ile ser arg arg ile pro arg ser his arg ile	

SEQ ID No.1B'

FIGURE 1B'

Seq1C: Insert of the DP428 clone, other reading frame

3/1 33/11
TCG CCT TTG ACG CCT ATT CGG TCG CGC AGC TTT TTG GCG ACG TCA CTG GTG CCC GCG TTG
ser pro leu thr pro ile arg ser arg ser phe leu ala thr ser leu val pro ala leu
63/21 93/31
CGG GCG TCC AGC CGC AGC GAC ACC ACA TAC GGC CGG TCC GGT TGC GGG GGC CGT TGG GTG
arg ala ser ser arg ser asp thr thr tyr gly arg ser gly cys gly gly arg trp val
123/41 153/51
GGG TTG GGT GCC TCC GTC ACC CCA GGC AGT TCG CTG GCT ATT TGT CGC AGT AGC GCG ACG
gly leu gly ala ser val thr pro gly ser ser leu ala ile cys arg ser ser ala thr
183/61 213/71
GCA TTG TCG ATG TCT TGG TAG CTA GCA TCC GGT CGG GGG GCC GCT ACC AGC GCC AGC GCC
ala leu ser met ser trp AMB leu ala ser gly arg gly ala ala thr ser ala ser ala
243/81 273/91
GGG GCT CCC CGG TCC GGG TAG TGC GCG TCG AGT TGG TCG TGG ACC AGC AAT GAC TGC GAC
gly ala pro arg ser gly AMB cys ala ser ser trp ser trp thr ser asn asp cys asp
303/101 333/111
CCG GCG ACT TCG AAA CCG CCA CCG GTT AGA TTC CCC GAC TGC GTC ATC GCC AGG TAA ACC
pro ala thr ser lys pro pro pro val arg phe pro asp cys val ile ala arg OCH thr
363/121 393/131
GCC GGC ACT AAC GCC AGC AAC CAA CCC GTG AAG ACC AAC CAA CGG CAC CTG CGC AGG TTG
ala gly thr asn ala ser asn gln pro val lys thr asn gln arg his leu arg arg leu
423/141 453/151
CGG CTC AAC CGC ATC ATG AAC TGC TGG ATT TCG GAC TCC CCG TAC TCT CGC GCA GTG CGT
arg leu asn arg ile met asn cys trp ile ser asp ser pro tyr ser arg ala val arg
483/161 513/171
GCC CGC GAG CCT ACC GAA GAT CGC GTG CAT GCG TTC GGC GTG GAC CGC ACA GCA CCT GGA
ala arg glu pro thr glu asp arg val his ala phe gly val asp arg thr ala pro gly
543/181 573/191
GTT GGC GGC GCC GAG GGC CGA GAT GGC AGG ATG ACG GAT CGT CGG GGG CGG GAA CTC CCA
val gly gly ala glu gly arg asp gly arg met thr asp arg arg gly arg glu leu pro
603/201 633/211
GGC CGC CGG ACC GTC GCA AAC CCG TCG CAA ACC CGT CGC AAA CCG TAA GGA GTC ATC CAT
gly arg arg thr val ala asn pro ser gln thr arg arg lys pro OCH gly val ile his
663/221 693/231
GAA GAC AGG CAC CGC GAC GAC GCG GCG CAG GCT GTT GGC AGT ACT GAT CGC CCT CGC GTT
glu asp arg his arg asp asp ala ala gln ala val gly ser thr asp arg pro arg val
723/241 753/251
GCC GGG GGC CGC CGT TGC GCT GCT GGC CGA ACC ATC AGC GAC CGG CGC GTC GGA CCC GTG
ala gly gly arg arg cys ala ala gly arg thr ile ser asp arg arg val gly pro val
783/261 813/271
CGC GGC CAG CGA AGT GGC GAG GAC GGT CGG TTC GGT CGC CAA GTC GAT GGG CGA CTA CCT
arg gly gln arg ser gly glu asp gly arg phe gly arg gln val asp gly arg leu pro
843/281 873/291
GGA TTC ACA CCC AGA GAC CAA CCA GGT GAT GAC CGC GGT CTT GCA GCA GCA GGT AGG GCC
gly phe thr pro arg asp gln pro gly asp asp arg gly leu ala ala ala gly arg ala
903/301 933/311
GGG GTC GGT CGC ATC GCT GAA GGC CCA TTT CGA GGC GAA TCC CAA GGT CGC ATC GGA TC
gly val gly arg ile ala glu gly pro phe arg gly glu ser gln gly arg ile gly

SEQ ID No.1C'

FIGURE 1C'

5/185

Coding sequence DP428 identical to the Rv0203 predicted by Cole et al.
(Nature 393:537-544)

1/1	31/11
ATG AAG ACA GGC ACC GCG ACG ACG CGG CGC	AGG CTG TTG GCA GTA CTG ATC GCC CTC GCG
Met lys thr gly thr ala thr thr arg arg	arg leu leu ala val leu ile ala leu ala
61/21	91/31
TTG CCG GGG GCC GCC GTT GCG CTG CTG GCC	GAA CCA TCA GCG ACC GGC GCG TCG GAC CCG
leu pro gly ala ala val ala leu leu ala	glu pro ser ala thr gly ala ser asp pro
121/41	151/51
TGC GCG GCC AGC GAA GTG GCG AGG ACG GTC	GGT TCG GTC GCC AAG TCG ATG GGC GAC TAC
cys ala ala ser glu val ala arg thr val	gly ser val ala lys ser met gly asp tyr
181/61	211/71
CTG GAT TCA CAC CCA GAG ACC AAC CAG GTG	ATG ACC GCG GTC TTG CAG CAG CAG GTA GGG
leu asp ser his pro glu thr asn gln val	met thr ala val leu gln gln gln val gly
241/81	271/91
CCG GGG TCG GTC GCA TCG CTG AAG GCC CAT	TTC GAG GCG AAT CCC AAG GTC GCA TCG GAT
pro gly ser val ala ser leu lys ala his	phe glu ala asn pro lys val ala ser asp
301/101	331/111
CTG CAC GCG CTT TCG CAA CCG CTG ACC GAT	CTT TCG ACT CGG TGC TCG CTG CCG ATC AGC
leu his ala leu ser gln pro leu thr asp	leu ser thr arg cys ser leu pro ile ser
361/121	391/131
GGC CTG CAG GCG ATC GGT TTG ATG CAG GCG	GTG CAG GGC GCC CGC CGG TAG
gly leu gln ala ile gly leu met gln ala val	gln gly ala arg arg AMB

SEQ ID No.1D

FIGURE 1D

ORF containing the DP428 sequence and forming part of seq1A'

1/1	31/11
TGA CGG ATC GTC GGG GGC GGG AAC TCC CAG	GCC GCC GGA CCG TCG CAA ACC CGT CGC AAA
OPA arg ile val gly gly gly asn ser gln	ala ala gly pro ser gln thr arg arg lys
61/21	91/31
CCC GTC GCA AAC CGT AAG GAG TCA TCC ATG	AAG ACA GGC ACC GCG ACG ACG CGG CGC AGG
pro val ala asn arg lys glu ser ser met	lys thr gly thr ala thr thr arg arg arg
121/41	151/51
CTG TTG GCA GTA CTG ATC GCC CTC GCG TTG	CCG GGG GCC GCC GTT GCG CTG CTG GCC GAA
leu leu ala val leu ile ala leu ala leu	pro gly ala ala val ala leu leu ala glu
181/61	211/71
CCA TCA GCG ACC GGC GCG TCG GAC CCG TGC	GCG GCC AGC GAA GTG GCG AGG ACG GTC GGT
pro ser ala thr gly ala ser asp pro cys	ala ala ser glu val ala arg thr val gly
241/81	271/91
TCG GTC GCC AAG TCG ATG GGC GAC TAC CTG	GAT TCA CAC CCA GAG ACC AAC CAG GTG ATG
ser val ala lys ser met gly asp tyr leu	asp ser his pro glu thr asn gln val met
301/101	331/111
ACC GCG GTC TTG CAG CAG CAG GTA GGG CCG	GGG TCG GTC GCA TCG CTG AAG GCC CAT TTC
thr ala val leu gln gln gln val gly pro	gly ser val ala ser leu lys ala his phe
361/121	391/131
GAG GCG AAT CCC AAG GTC GCA TCG GAT CTG	CAC GCG CTT TCG CAA CCG CTG ACC GAT CTT
glu ala asn pro lys val ala ser asp leu	his ala leu ser gln pro leu thr asp leu
421/141	451/151
TCG ACT CGG TGC TCG CTG CCG ATC AGC GGC	CTG CAG GCG ATC GGT TTG ATG CAG GCG GTG
ser thr arg cys ser leu pro ile ser gly leu	gln ala ile gly leu met gln ala val
481/161	
CAG GGC GCC CGC CGG TAG	
gln gly ala arg arg AMB	

SEQ ID No.1F

FIGURE 1F

491 CCGGTCGGGGGGCCGCTACCAGCGCCAGCGCCGGGGCTCCCCGGTCCGGGTA GTG CGC GTC GAG TTG GTC GTG 563
1 V R V E L V V 7

564 GAC CAG CAA TGA CTGCGACCCGGCGACTTCGAAACCGCCACCGGTTAGATTCCCCGACTGCGTCATCGCCAGGTAA 639
8 D Q Q *

640 ACCGCCGGGCACTAACGCCAGCAACCAACCC GTG AAG ACC AAC CAA CGG CAC CTG CGC AGG TTG CGG 705
1 V K T N Q R H L R R L R 12

706 CTC AAC CGC ATC ATG AAC TGC TGG ATT TCG GAC TCC CCG TAC TCT CGC GCA GTG CGT GCC 765
13 L N R I M N C W I S D S P Y S R A V R A 32

766 CGC GAG CCT ACC GAA GAT CGC GTG CAT GCG TTC GGC GTG GAC CGC ACA GCA CCT GGA GTT 825
33 R E P T E D R V H A F G V D R T A P G V 52

826 GGC GGC GCC GAG GGC CGA GAT GGC AGG ATG ACG GAT CGT CGG GGG CGG GAA CTC CCA GGC 885
53 G G A E G R D G R M T D R R G R E L P G 72

886 CGC CGG ACC GTC GCA AAC CCG TCG CAA ACC CGT CGC AAA CCG TAA GGAGTCATCC ATG AAG 946
73 R R T V A N P S Q T R R K P * xxxxxx M K 2

947 ACA GGC ACC GCG ACG ACG CGG CGC AGG CTG TTG GCA GTA CTG ATC GCC CTC GCG TTG CCG 1006
3 T G T A T T R R R L L A V L I A L A L P 22

1007 GGG GCC GCC GTT GCG CTG CTG GCC GAA CCA TCA GCG ACC GGC GCG TCG GAC CCG TGC GCG 1066
23 G A A V A L L A E P S A T G A S D P C A 42

1067 GCC AGC GAA GTG GCG AGG ACG GTC GGT TCG GTC GCC AAG TCG ATG GGC GAC TAC CTG GAT 1126
43 A S E V A R T V G S V A K S M G D Y L D 62

1127 TCA CAC CCA GAG ACC AAC CAG GTG ATG ACC GCG GTC TTG CAG CAG CAG GTA GGG CCG GGG 1186
63 S H P E T N Q V M T A V L Q Q Q V G P G 82

1187 TCG GTC GCA TCG CTG AAG GCC CAT TTC GAG GCG AAT CCC AAG GTC GCA TCG GAT CTG CAC 1246
83 S V A S L K A H F E A N P K V A S D L H 102

1247 GCG CTT TCG CAA CCG CTG ACC GAT CTT TCG ACT CGG TGC TCG CTG CCG ATC AGC GGC CTG 1306
103 A L S Q P L T D L S T R C S L P I S G L 122

1307 CAG GCG ATC GGT TTG ATG CAG GCG GTG CAG GGC GCC CGC CGG TAG ATG CCG GAC CGC CGC 1366
123 Q A I G L M Q A V Q G A R R * M P D R R 5

1367 CGG GTC CGG CGC AGT CGA CGT GAG GCA GCG GTC GCC TAC CGG GGC GGT GTC TCG CCG CCT 1426
6 R V R R S R R E A A V A Y R G G V S P P 25

1427 TCT GGT CGC AGG TCA GGG GTC GGC GCT GGA CCT TGC GGT GTG GTT TCG ACC GGG TCG TCG 1486
26 S G R R S G V G A G P C G V V S T G S S 45

1487 CAG GGT GTG CCC TGC GGT TGG ATG ACA AGT CGC AGG TTT GGA TCG GTT GGC GGG TCG CGA 1546
46 Q G V P C G W M T S R R F G S V G G S R 65

1547 TCG TTG T 1553
66 S L 67

SEQ ID No.2

FIGURE 2

31/11
 TCG CCG GCT CGC GGA CGT AGA TAA TAG CTC ACC GTT GGA CGA CCT CGA CAG GGT CCT TTG
 ser pro ala arg gly arg arg OCH AMB leu thr val gly arg pro arg gln gly pro leu
 61/21
 91/31
 TGA CTG CCG GGC TTG ACG CGG ACG ACC ACA GAG TCG GGT CAT CGC CTA AGG CTA CCG TTC
 OPA leu pro gly leu thr arg thr thr thr glu ser gly his arg leu arg leu pro phe
 121/41
 151/51
 TGA CCT GGG GTG CGT GGG CGC CGA CGA GTG AGG CAG TCA TGT CTC AGG GCC CAC CGC CAC
 OPA pro gly val arg gly arg arg arg val arg gln ser cys leu arg ala his arg his
 181/61
 211/71
 CTC GGT CGC CGG CAG TGT CAG CAT GTG CAG ATG ACT CCA CGC AGC TTG TTC GTG TTG GTG
 leu gly arg arg gln cys gln his val gln met thr pro arg ser leu phe val leu val
 241/81
 271/91
 TCG TGG TTG CGA CGA CTT GGC GCT GGT GAG CGC ACC CGC CGG CGT CGT GCC GCG CAT GCG
 ser trp leu arg arg leu gly ala gly glu arg thr arg arg arg arg ala ala his ala
 301/101
 GAT C
 asp

SEQ ID No.3A

FIGURE 3A

32/11
 CGC CGG CTC GCG GAC GTA GAT AAT AGC TCA CCG TTG GAC GAC CTC GAC AGG GTC CTT TGT
 arg arg leu ala asp val asp asn ser ser pro leu asp asp leu asp arg val leu cys
 62/21
 92/31
 GAC TGC CGG GCT TGA CGC GGA CGA CCA CAG AGT CGG GTC ATC GCC TAA GGC TAC CGT TCT
 asp cys arg ala OPA arg gly arg pro gln ser arg val ile ala OCH gly tyr arg ser
 122/41
 152/51
 GAC CTG GGG TGC GTG GGC GCC GAC GAG TGA GGC AGT CAT GTC TCA GGG CCC ACC GCC ACC
 asp leu gly cys val gly ala asp glu OPA gly ser his val ser gly pro thr ala thr
 182/61
 212/71
 TCG GTC GCC GGC AGT GTC AGC ATG TGC AGA TGA CTC CAC GCA GCT TGT TCG TGT TGG TGT
 ser val ala gly ser val ser met cys arg OPA leu his ala ala cys ser cys trp cys
 242/81
 272/91
 CGT GGT TGC GAC GAC TTG GCG CTG GTG AGC GCA CCC GCC GGC GTC GTG CCG CGC ATG CGG
 arg gly cys asp asp leu ala leu val ser ala pro ala gly val val pro arg met arg
 302/101
 ATC
 ile

SEQ ID No.3B

FIGURE 3B

33/11
 GCC GGC TCG CGG ACG TAG ATA ATA GCT CAC CGT TGG ACG ACC TCG ACA GGG TCC TTT GTG
 ala gly ser arg thr AMB ile ile ala his arg trp thr thr ser thr gly ser phe val
 63/21 93/31
 ACT GCC GGG CTT GAC GCG GAC GAC CAC AGA GTC GGG TCA TCG CCT AAG GCT ACC GTT CTG
 thr ala gly leu asp ala asp asp his arg val gly ser ser pro lys ala thr val leu
 123/41 153/51
 ACC TGG GGT GCG TGG GCG CCG ACG AGT GAG GCA GTC ATG TCT CAG GGC CCA CCG CCA CCT
 thr trp gly ala trp ala pro thr ser glu ala val met ser gln gly pro pro pro pro
 183/61 213/71
 CGG TCG CCG GCA GTG TCA GCA TGT GCA GAT GAC TCC ACG CAG CTT GTT CGT GTT GGT GTC
 arg ser pro ala val ser ala cys ala asp asp ser thr gln leu val arg val gly val
 243/81 273/91
 GTG GTT GCG ACG ACT TGG CGC TGG TGA GCG CAC CCG CCG GCG TCG TGC CGC GCA TGC GGA
 val val ala thr thr trp arg trp OPA ala his pro pro ala ser cys arg ala cys gly

TC

SEQ ID No.3C

FIGURE 3C

31/11
 CCA ATT TTC CTT CGC GCC GTG CAA TAC CAT CTG CAA GAC CAG CGA CGG CCC GTG GTT GCG
 pro ile phe leu arg ala val gln tyr his leu gln asp gln arg arg pro val val ala
 61/21 91/31
 GTC GCG CAG CTT GCG GAA ACC GGG TAT GGA CCC TGC CGT ACC GTT GTT GCC ACT TGA TGT
 val ala gln leu ala glu thr gly tyr gly pro cys arg thr val val ala thr OPA cys
 121/41 151/51
 CGT CGC TCT CCA CCC GTC GGG GGG CGA AAG CCA TTC CGA CAC TGG GAT CCT CAA AAC GTC
 arg arg ser pro pro val gly gly arg lys pro phe arg his trp asp pro gln asn val
 181/61 211/71
 GGC TGA GTG TCT GCA GGG CTC CGG GGA GCA GCC GAT CAT CAC CAT GTA CGA ACT GAA TAA
 gly OPA val ser ala gly leu arg gly ala ala asp his his his val arg thr glu OCH
 241/81 271/91
 GTC CCC CGC GCG CGA CTT CCA GAC ATT TGT TGT GGT TTC GGT TGA GGC CGA GGC GAG GCT
 val pro arg ala arg leu pro asp ile cys cys gly phe gly OPA gly arg gly glu ala
 301/101 331/111
 CAT TTC GCA GCA ACC GGT CTC CGG GTC GCA GCA TCG TTG CGG CGA TCG CGG CGC AGT CGT
 his phe ala ala thr gly leu arg val ala ala ser leu arg arg ser arg arg ser arg
 361/121
 CGG ACG AGT CGT CGT CAA CGA CCA CGA TC
 arg thr ser arg arg gln arg pro arg

SEQ ID No.4A

FIGURE 4A

32/11
 CAA TTT TCC TTC GCG CCG TGC AAT ACC ATC TGC AAG ACC AGC GAC GGC CCG TGG TTG CGG
 gln phe ser phe ala pro cys asn thr ile cys lys thr ser asp gly pro trp leu arg
 62/21 92/31
 TCG CGC AGC TTG CCG AAA CCG GGT ATG GAC CCT GCC GTA CCG TTG TTG CCA CTT GAT GTC
 ser arg ser leu arg lys pro gly met asp pro ala val pro leu leu pro leu asp val
 122/41 152/51
 GTC GCT CTC CAC CCG TCG GGG GGC GAA AGC CAT TCC GAC ACT GGG ATC CTC AAA ACG TCG
 val ala leu his pro ser gly gly glu ser his ser asp thr gly ile leu lys thr ser
 182/61 212/71
 GCT GAG TGT CTG CAG GGC TCC GGG GAG CAG CCG ATC ATC ACC ATG TAC GAA CTG AAT AAG
 ala glu cys leu gln gly ser gly glu gln pro ile ile thr met tyr glu leu asn lys
 242/81 272/91
 TCC CCC GCG CGC GAC TTC CAG ACA TTT GTT GTG GTT TCG GTT GAG GCC GAG GCG AGG CTC
 ser pro ala arg asp phe gln thr phe val val val ser val glu ala glu ala arg leu
 302/101 332/111
 ATT TCG CAG CAA CCG GTC TCC GGG TCG CAG CAT CGT TGC GGC GAT CGC GGC GCA GTC GTC
 ile ser gln gln pro val ser gly ser gln his arg cys gly asp arg gly ala val val
 362/121
 GGA CGA GTC GTC GTC AAC GAC CAC GAT C
 gly arg val val val asn asp his asp

SEQ ID No.4B

FIGURE 4B

33/11
 AAT TTT CCT TCG CGC CGT GCA ATA CCA TCT GCA AGA CCA GCG ACG GCC CGT GGT TGC GGT
 asn phe pro ser arg arg ala ile pro ser ala arg pro ala thr ala arg gly cys gly
 63/21 93/31
 CGC GCA GCT TGC GGA AAC CGG GTA TGG ACC CTG CCG TAC CGT TGT TGC CAC TTG ATG TCG
 arg ala ala cys gly asn arg val trp thr leu pro tyr arg cys cys his leu met ser
 123/41 153/51
 TCG CTC TCC ACC CGT CGG GGG GCG AAA GCC ATT CCG ACA CTG GGA TCC TCA AAA CGT CGG
 ser leu ser thr arg arg gly ala lys ala ile pro thr leu gly ser ser lys arg arg
 183/61 213/71
 CTG AGT GTC TGC AGG GCT CCG GGG AGC AGC CGA TCA TCA CCA TGT ACG AAC TGA ATA AGT
 leu ser val cys arg ala pro gly ser ser arg ser ser pro cys thr asn OPA ile ser
 243/81 273/91
 CCC CCG CGC GCG ACT TCC AGA CAT TTG TTG TGG TTT CGG TTG AGG CCG AGG CGA GGC TCA
 pro pro arg ala thr ser arg his leu leu trp phe arg leu arg pro arg arg gly ser
 303/101 333/111
 TTT CGC AGC AAC CGG TCT CCG GGT CGC AGC ATC GTT GCG GCG ATC GCG GCG CAG TCG TCG
 phe arg ser asn arg ser pro gly arg ser ile val ala ala ile ala ala gln ser ser
 363/121
 GAC GAG TCG TCG TCA ACG ACC ACG ATC
 asp glu ser ser ser thr thr thr ile

SEQ ID No.4C

FIGURE 4C

10/185

part of the nucleotide sequence of seq4A

```
1/1                               31/11
CCG CGC GCG ACT TCC AGA CAT TTG TTG TGG TTT CGG TTG AGG CCG AGG CGA GGC TCA TTT
pro arg ala thr ser arg his leu leu trp phe arg leu arg pro arg arg gly ser phe
61/21                               91/31
CGC AGC AAG CGG TCT CCG GGT CGC AGC ATC GTT GCG GCG ATC GCG GCG CAG TCG TCG GAC
arg ser lys arg ser pro gly arg ser ile val ala ala ile ala ala gln ser ser asp
121/41
GAG TCG TCG TCA ACG ACC ACG ATC
glu ser ser ser thr thr thr ile
```

SEQ ID No.4A'

FIGURE 4A'

```
1/1                               31/11
CGC GCG CGA CTT CCA GAC ATT TGT TGT GGT TTC GGT TGA GGC CGA GGC GAG GCT CAT TTC
arg ala arg leu pro asp ile cys cys gly phe gly OPA gly arg gly glu ala his phe
61/21                               91/31
GCA GCA AGC GGT CTC CGG GTC GCA GCA TCG TTG CGG CGA TCG CGG CGC AGT CGT CGG ACG
ala ala ser gly leu arg val ala ala ser leu arg arg ser arg arg ser arg arg thr
121/41
AGT CGT CGT CAA CGA CCA CGA TC
ser arg arg gln arg pro arg
```

SEQ ID No.4B'

FIGURE 4B'

```
1/1                               31/11
GCC GCG CGC GAC TTC CAG ACA TTT GTT GTG GTT TCG GTT GAG GCC GAG GCG AGG CTC ATT
ala ala arg asp phe gln thr phe val val val ser val glu ala glu ala arg leu ile
61/21                               91/31
TCG CAG CAA GCG GTC TCC GGG TCG CAG CAT CGT TGC GGC GAT CGC GGC GCA GTC GTC GGA
ser gln gln ala val ser gly ser gln his arg cys gly asp arg gly ala val val gly
121/41
CGA GTC GTC GTC AAC GAC CAC GAT C
arg val val val asn asp his asp
```

SEQ ID No.4C'

FIGURE 4C'

11/185

ORF according to Cole et al. (Nature 393:537-544) and containing the sequence Seq 4A'

1/1 31/11
tga ata agt ccg ccg cgc gcg act tcc aga cat ttg ttg tgg ttt cgg ttg agg ccg agg
OPA ile ser pro pro arg ala thr ser arg his leu leu trp phe arg leu arg pro arg
61/21 91/31
cga ggc tca ttt cgc agc aag cgg tct ccg ggt cgc agc atc gtt gcg gcg atc gcg gcg
arg gly ser phe arg ser lys arg ser pro gly arg ser ile val ala ala ile ala ala
121/41 151/51
cag tcg tcg gac gag tcg tcg tca acg acc acg atc tcg aac tcg acg ccc tcc tgt tcg
gln ser ser asp glu ser ser ser thr thr thr ile ser asn ser thr pro ser cys ser
181/61 211/71
agg atg cta cgc aga cag cgc tcg atg gtg gcg ccg ttg ttg tac atc ggg atg cac acc
arg met leu arg arg gln arg ser met val ala pro leu leu tyr ile gly met his thr
241/81 271/91
gag ata agc ggt ttc gcc ggg ttc acc gat acc acg ctt gat gca tca cca ggc acc aca
glu ile ser gly phe ala gly phe thr asp thr thr leu asp ala ser pro gly thr thr
301/101
tgg cga ctc aga gac tag
trp arg leu arg asp AMB

SEQ ID No.4F

FIGURE 4F

sequence upstream of seq4A' and fused with seq4A'

1/1 31/11
GCA ACC TAC CAG CAG AGC CAG GGG CTC ACA GGA CCT AAA GGA GTA GCG CCC ATG GCT GAT
ala thr tyr gln gln ser gln gly leu thr gly pro lys gly val ala pro met ala asp

C

SEQ ID No.4J

FIGURE 4J

seq4J' in another reading frame

1/1 31/11
ACG CAA CCT ACC AGC AGA GCC AGG GGC TCA CAG GAC CTA AAG GAG TAG CGC CCA TGG CTG
thr gln pro thr ser arg ala arg gly ser gln asp leu lys glu AMB arg pro trp leu
61/21
ATC
ile

SEQ ID N°4K

FIGURE 4K

seq 4J' in the third reading frame

1/1 31/11
CGC AAC CTA CCA GCA GAG CCA GGG GCT CAC AGG ACC TAA AGG AGT AGC GCC CAT GGC TGA
arg asn leu pro ala glu pro gly ala his arg thr OCH arg ser ser ala his gly OPA

TC

SEQ ID No.4L

FIGURE 4L

sequence Rv2050 predicted by Cole et al. (Nature 393:537-544) and containing seq4J

1/1	31/11
ATG GCT GAT CGT GTC CTG AGG GGC AGT CGC	CTC GGA GCC GTG AGC TAT GAG ACC GAC CGC
Met ala asp arg val leu arg gly ser arg	leu gly ala val ser tyr glu thr asp arg
61/21	91/31
AAC CAC GAC CTG GCG CCG CGC CAG ATC GCG	CGG TAC CGC ACC GAC AAC GGC GAG GAG TTC
asn his asp leu ala pro arg gln ile ala	arg tyr arg thr asp asn gly glu glu phe
121/41	151/51
GAA GTC CCG TTC GCC GAT GAC GCC GAG ATC	CCC GGC ACC TGG TTG TGC CGC AAC GGC ATG
glu val pro phe ala asp asp ala glu ile	pro gly thr trp leu cys arg asn gly met
181/61	211/71
GAA GGC ACC CTG ATC GAG GGC GAC CTG CCC	GAG CCG AAG AAG GTT AAG CCG CCC CGG ACG
glu gly thr leu ile glu gly asp leu pro	glu pro lys lys val lys pro pro arg thr
241/81	271/91
CAC TGG GAC ATG CTG CTG GAG CGC CGT TCC	ATC GAA GAA CTC GAA GAG TTA CTT AAG GAG
his trp asp met leu leu glu arg arg ser	ile glu glu leu glu glu leu leu lys glu
301/101	331/111
CGC CTC GAG CTC ATT CGG TCA CGT CGG CGC	GGC TGA
arg leu glu leu ile arg ser arg arg arg	gly OPA

SEQ ID No.4M

FIGURE 4M

ORF according to Cole et al. (Nature 393:537-544) and containing the sequence Rv2050

1/1	31/11
TAG TCC GCC CGG GTG TCC GAT CCC GGT ATC	ATT GAT GGT CGC GCC GCG CGC GTC GCG TGC
AMB ser ala arg val ser asp pro gly ile	ile asp gly arg ala ala arg val ala cys
61/21	91/31
CGG GAA CTA CGC AGA CGG CCG CAG CGT TTG	CCA ACC GGA GCC AGT CGC CAG TAC GCA ACC
arg glu leu arg arg arg pro gln arg leu	pro thr gly ala ser arg gln tyr ala thr
121/41	151/51
TAC CAG CAG AGC CCA GGG CTC ACA GGA CCT	AAA GGA GTA GCG CCC ATG GCT GAT CGT GTC
tyr gln gln ser pro gly leu thr gly pro	lys gly val ala pro met ala asp arg val
181/61	211/71
CTG AGG GGC AGT CGC CTC GGA GCC GTG AGC	TAT GAG ACC GAC CGC AAC CAC GAC CTG GCG
leu arg gly ser arg leu gly ala val ser	tyr glu thr asp arg asn his asp leu ala
241/81	271/91
CCG CGC CAG ATC GCG CGG TAC CGC ACC GAC	AAC GGC GAG GAG TTC GAA GTC CCG TTC GCC
pro arg gln ile ala arg tyr arg thr asp	asn gly glu glu phe glu val pro phe ala
301/101	331/111
GAT GAC GCC GAG ATC CCC GGC ACC TGG TTG	TGC CGC AAC GGC ATG GAA GGC ACC CTG ATC
asp asp ala glu ile pro gly thr trp leu	cys arg asn gly met glu gly thr leu ile
361/121	391/131
GAG GGC GAC CTG CCC GAG CCG AAG AAG GTT	AAG CCG CCC CGG ACG CAC TGG GAC ATG CTG
glu gly asp leu pro glu pro lys lys val	lys pro pro arg thr his trp asp met leu
421/141	451/151
CTG GAG CGC CGT TCC ATC GAA GAA CTC GAA	GAG TTA CTT AAG GAG CGC CTC GAG CTC ATT
leu glu arg arg ser ile glu glu leu glu	glu leu leu lys glu arg leu glu leu ile
481/161	
CGG TCA CGT CGG CGC GGC TGA	
arg ser arg arg arg gly OPA	

SEQ ID No.4N

FIGURE 4

13/185

31/11
GAT CGC GGT CAA CGA GGC CGA ATA CGG CGA GAT GTG GGC CCA AGA CGC CGC CGC GAT GTT
asp arg gly gln arg gly arg ile arg arg asp val gly pro arg arg arg arg asp val
61/21 91/31
TGG CTA CGC CGC GGC GAC GGC GAC GGC GAC GGC GAC GTT GCT GCC GTT CGA GGA GGC GCC
trp leu arg arg gly asp gly asp gly asp gly asp val ala ala val arg gly gly ala
121/41 151/51
GGA GAT GAC CAG CGC GGG TGG GCT CCT CGA GCA GGC CGC CGC GGT CGA GGA GGC CTC CGA
gly asp asp gln arg gly trp ala pro arg ala gly arg arg gly arg gly gly leu arg
181/61 211/71
CAC CGC CGC GGC GAA CCA GTT GAT GAA CAA TGT GCC CCA GGC GCT GCA ACA GCT GGC CCA
his arg arg gly glu pro val asp glu gln cys ala pro gly ala ala thr ala gly pro
241/81 271/91
GCC CAC GCA GGG CAC CAC GCC TTC TTC CAA GCT GGG TGG CCT GTG GAA GAC GGT CTC GCC
ala his ala gly his his ala phe phe gln ala gly trp pro val glu asp gly leu ala
301/101
GCA TCG GTC GCC GAT C
ala ser val ala asp

SEQ ID No.5A

FIGURE 5A

32/11
ATC GCG GTC AAC GAG GCC GAA TAC GGC GAG ATG TGG GCC CAA GAC GCC GCC GCG ATG TTT
ile ala val asn glu ala glu tyr gly glu met trp ala gln asp ala ala ala met phe
62/21 92/31
GGC TAC GCC GCG GCG ACG GCG ACG GCG ACG GCG ACG TTG CTG CCG TTC GAG GAG GCG CCG
gly tyr ala ala ala thr ala thr ala thr ala thr leu leu pro phe glu glu ala pro
122/41 152/51
GAG ATG ACC AGC GCG GGT GGG CTC CTC GAG CAG GCC GCC GCG GTC GAG GAG GCC TCC GAC
glu met thr ser ala gly gly leu leu glu gln ala ala ala val glu glu ala ser asp
182/61 212/71
ACC GCC GCG GCG AAC CAG TTG ATG AAC AAT GTG CCC CAG GCG CTG CAA CAG CTG GCC CAG
thr ala ala ala asn gln leu met asn asn val pro gln ala leu gln gln leu ala gln
242/81 272/91
CCC ACG CAG GGC ACC ACG CCT TCT TCC AAG CTG GGT GGC CTG TGG AAG ACG GTC TCG CCG
pro thr gln gly thr thr pro ser ser lys leu gly gly leu trp lys thr val ser pro
302/101
CAT CGG TCG CCG ATC
his arg ser pro ile

SEQ ID No.5B

FIGURE 5B

33/11
 TCG CGG TCA ACG AGG CCG AAT ACG GCG AGA TGT GGG CCC AAG ACG CCG CCG CGA TGT TTG
 ser arg ser thr arg pro asn thr ala arg cys gly pro lys thr pro pro arg cys leu
 63/21
 GCT ACG CCG CGG CGA CGG CGA CGG CGA CGG CGA CGT TGC TGC CGT TCG AGG AGG CGC CGG
 ala thr pro arg arg arg arg arg arg arg arg arg arg arg cys cys arg ser arg arg arg arg
 123/41
 AGA TGA CCA GCG CGG GTG GGC TCC TCG AGC AGG CCG CCG CGG TCG AGG AGG CCT CCG ACA
 arg OPA pro ala arg val gly ser ser ser arg pro pro arg ser arg arg pro pro thr
 183/61
 CCG CCG CGG CGA ACC AGT TGA TGA ACA ATG TGC CCC AGG CGC TGC AAC AGC TGG CCC AGC
 pro pro arg arg thr ser OPA OPA thr met cys pro arg arg cys asn ser trp pro ser
 243/81
 273/91
 CCA CGC AGG GCA CCA CGC CTT CTT CCA AGC TGG GTG GCC TGT GGA AGA CGG TCT CGC CGC
 pro arg arg ala pro arg leu leu pro ser trp val ala cys gly arg arg ser arg arg
 303/101
 ATC GGT CGC CGA TC
 ile gly arg arg

SEQ ID No.5C

FIGURE 5C

part of the nucleotide sequence Seq 5A

1/1
 CGC CGC GGC GAC GGC GAC GGC GAC GGC GAC GTT GCT GCC GTT CGA GGA GGC GCC GGA GAT
 arg arg gly asp gly asp gly asp gly asp val ala ala val arg gly gly ala gly asp
 61/21
 GAC CAG CGC GGG TGG GCT CCT CGA GCA GGC CGC CGC GGT CGA GGA GGC CTC CGA CAC CGC
 asp gln arg gly trp ala pro arg ala gly arg arg gly arg gly gly leu arg his arg
 121/41
 CGC GGC GAA CCA GTT GAT GAA CAA TGT GCC CCA GGC GCT GCA ACA GCT GGC CCA GCC CAC
 arg gly glu pro val asp glu gln cys ala pro gly ala ala thr ala gly pro ala his
 181/61
 GCA GGG CAC CAC GCC TTC TTC CAA GCT GGG TGG CCT GTG GAA GAC GGT CTC GCC GCA TCG
 ala gly his his ala phe phe gln ala gly trp pro val glu asp gly leu ala ala ser
 241/81
 GTC GCC GAT C
 val ala asp

SEQ ID No.5A'

FIGURE 5A'

1/1 31/11
TAC GCC GCG GCG ACG GCG ACG GCG ACG GCG ACG TTG CTG CCG TTC GAG GAG GCG CCG GAG
tyr ala ala ala thr ala thr ala thr ala thr leu leu pro phe glu glu ala pro glu
61/21 91/31
ATG ACC AGC GCG GGT GGG CTC CTC GAG CAG GCC GCC GCG GTC GAG GAG GCC TCC GAC ACC
met thr ser ala gly gly leu leu glu gln ala ala ala val glu glu ala ser asp thr
121/41 151/51
GCC GCG GCG AAC CAG TTG ATG AAC AAT GTG CCC CAG GCG CTG CAA CAG CTG GCC CAG CCC
ala ala ala asn gln leu met asn asn val pro gln ala leu gln gln leu ala gln pro
181/61 211/71
ACG CAG GGC ACC ACG CCT TCT TCC AAG CTG GGT GGC CTG TGG AAG ACG GTC TCG CCG CAT
thr gln gly thr thr pro ser ser lys leu gly gly leu trp lys thr val ser pro his
241/81
CGG TCG CCG ATC
arg ser pro ile

SEQ ID No.5B'

FIGURE 5B'

1/1 31/11
ACG CCG CGG CGA CGG CGA CGG CGA CGG CGA CGT TGC TGC CGT TCG AGG AGG CGC CGG AGA
thr pro arg arg arg arg arg arg arg arg arg arg cys cys arg ser arg arg arg arg
61/21 91/31
TGA CCA GCG CGG GTG GGC TCC TCG AGC AGG CCG CCG CGG TCG AGG AGG CCT CCG ACA CCG
OPA pro ala arg val gly ser ser ser arg pro pro arg ser arg arg pro pro thr pro
121/41 151/51
CCG CGG CGA ACC AGT TGA TGA ACA ATG TGC CCC AGG CGC TGC AAC AGC TGG CCC AGC CCA
pro arg arg thr ser OPA OPA thr met cys pro arg arg cys asn ser trp pro ser pro
181/61 211/71
CGC AGG GCA CCA CGC CTT CTT CCA AGC TGG GTG GCC TGT GGA AGA CGG TCT CGC CGC ATC
arg arg ala pro arg leu leu pro ser trp val ala cys gly arg arg ser arg arg ile
241/81
GGT CGC CGA TC
gly arg arg

SEQ ID No.5C'

FIGURE 5C'

ORF predicted by Cole et al. (Nature 393:537-544) and containing seq5A'

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1/1                               31/11
tga act gat gat tct gat agc gac caa cct ctt ggg gca aaa cac ccc ggc gat cgc ggt
OPA thr asp asp ser asp ser asp gln pro leu gly ala lys his pro gly asp arg gly
61/21                               91/31
caa cga ggc cga ata cgg cga gat gtg ggc cca aga cgc cgc cgc gat gtt tgg cta cgc
gln arg gly arg ile arg arg asp val gly pro arg arg arg arg asp val trp leu arg
121/41                               151/51
cgc ggc gac ggc gac ggc gac ggc gac gtt gct gcc gtt cga gga ggc gcc gga gat gac
arg gly asp gly asp gly asp gly asp val ala ala val arg gly gly ala gly asp asp
181/61                               211/71
cag cgc ggg tgg gct cct cga gca ggc cgc cgc ggt cga gga ggc ctc cga cac cgc cgc
gln arg gly trp ala pro arg ala gly arg arg gly arg gly gly leu arg his arg arg
241/81                               271/91
ggc gaa cca gtt gat gaa caa tgt gcc cca ggc gct gca aca gct ggc cca gcc cac gca
gly glu pro val asp glu gln cys ala pro gly ala ala thr ala gly pro ala his ala
301/101                               331/111
ggg cac cac gcc ttc ttc caa gct ggg tgg cct gtg gaa gac ggt ctc gcc gca tcg gtc
gly his his ala phe phe gln ala gly trp pro val glu asp gly leu ala ala ser val
361/121                               391/131
gcc gat cag caa cat ggt gtc gat ggc caa caa cca cat gtc gat gac caa ctc ggg tgt
ala asp gln gln his gly val asp gly gln gln pro his val asp asp gln leu gly cys
421/141                               451/151
gtc gat gac caa cac ctt gag ctc gat gtt gaa ggg ctt tgc tcc ggc ggc ggc cgc cca
val asp asp gln his leu glu leu asp val glu gly leu cys ser gly gly gly arg pro
481/161                               511/171
ggc cgt gca aac cgc ggc gca aaa cgg ggt ccg ggc gat gag ctc gct ggg cag ctc gct
gly arg ala asn arg gly ala lys arg gly pro gly asp glu leu ala gly gln leu ala
541/181                               571/191
ggg ttc ttc ggg tct ggg cgg tgg ggt ggc cgc caa ctt ggg tcg ggc ggc ctc ggt cgg
gly phe phe gly ser gly arg trp gly gly arg gln leu gly ser gly gly leu gly arg
601/201                               631/211
ttc gtt gtc ggt gcc gca ggc ctg ggc cgc ggc caa cca ggc agt cac ccc ggc ggc gcg
phe val val gly ala ala gly leu gly arg gly gln pro gly ser his pro gly gly ala
661/221                               691/231
ggc gct gcc gct gac cag cct gac cag cgc cgc gga aag agg gcc cgg gca gat gct ggg
gly ala ala ala asp gln pro asp gln arg arg gly lys arg ala arg ala asp ala gly
721/241                               751/251
cgg gct gcc ggt ggg gca gat ggg cgc cag ggc cgg tgg tgg gct cag tgg tgt gct gcg
arg ala ala gly gly ala asp gly arg gln gly arg trp trp ala gln trp cys ala ala
781/261                               811/271
tgt tcc gcc gcg acc cta tgt gat gcc gca ttc tcc ggc ggc cgg cta gga gag ggg gcg
cys ser ala ala thr leu cys asp ala ala phe ser gly gly arg leu gly glu gly ala
841/281
cag act gtc gtt att tga
gln thr val val ile OPA

```

SEQ ID No.5F

FIGURE 5F

sequence Rv1196 predicted by Cole et al. (Nature 393:537-544) and capable of encoding an ORF fused with Seq5A'

```

1/1
atg gtg gat ttc ggg gcg tta cca ccg gag atc aac tcc gcg agg atg tac gcc ggc ccg
Met val asp phe gly ala leu pro pro glu ile asn ser ala arg met tyr ala gly pro
61/21
ggg ttc gcc tgc ctg gtg gcc gcg gct cag atg tgg gac agc gtg gcg agt gac ctg ttt
gly ser ala ser leu val ala ala ala gln met trp asp ser val ala ser asp leu phe
121/41
tcg gcc gcg tgc gcg ttt cag tgc gtg gtc tgg ggt ctg acg gtg ggg tgc tgg ata ggt
ser ala ala ser ala phe gln ser val val trp gly leu thr val gly ser trp ile gly
181/61
tcg tgc gcg ggt ctg atg gtg gcg gcg gcc tgc ccg tat gtg gcg tgg atg agc gtc acc
ser ser ala gly leu met val ala
ala ala ser pro tyr val ala trp met ser val thr
241/81
gcg ggg cag gcc gag ctg acc gcc gcc cag gtc ccg gtt gct gcg gcg gcc tac gag acg
ala gly gln ala glu leu thr ala ala gln val arg val ala ala ala ala tyr glu thr
301/101
gcg tat ggg ctg acg gtg ccc ccg ccg gtg atc gcc gag aac cgt gct gaa ctg atg att
ala tyr gly leu thr val pro pro pro val ile ala glu asn arg ala glu leu met ile
361/121
ctg ata gcg acc aac ctc ttg ggg caa aac acc ccg gcg atc gcg gtc aac gag gcc gaa
leu ile ala thr asn leu leu gly gln asn thr pro ala ile ala val asn glu ala glu
421/141
tac ggc gag atg tgg gcc caa gac gcc gcc gcg atg ttt ggc tac gcc gcg gcg acg gcg
tyr gly glu met trp ala gln asp ala ala ala met phe gly tyr ala ala ala thr ala
481/161
acg gcg acg gcg acg ttg ctg ccg ttc gag gag gcg ccg gag atg acc agc gcg ggt ggg
thr ala thr ala thr leu leu pro phe glu glu ala pro glu met thr ser ala gly gly
541/181
ctc ctc gag cag gcc gcc gcg gtc gag gag gcc tcc gac acc gcc gcg gcg aac cag ttg
leu leu glu gln ala ala ala val glu glu ala ser asp thr ala ala ala asn gln leu
601/201
atg aac aat gtg ccc cag gcg ctg caa cag ctg gcc cag ccc acg cag ggc acc acg cct
met asn asn val pro gln ala leu gln gln leu ala gln pro thr gln gly thr thr pro
661/221
tct tcc aag ctg ggt ggc ctg tgg aag acg gtc tgc ccg cat cgg tgc ccg atc agc aac
ser ser lys leu gly gly leu trp lys thr val ser pro his arg ser pro ile ser asn
721/241
atg gtg tgc atg gcc aac aac cac atg tgc atg acc aac tgc ggt gtg tgc atg acc aac
met val ser met ala asn asn his met ser met thr asn ser gly val ser met thr asn
781/261
acc ttg agc tgc atg ttg aag ggc ttt gct ccg gcg gcg gcc gcc cag gcc gtg caa acc
thr leu ser ser met leu lys gly phe ala pro ala ala ala ala gln ala val gln thr
841/281
gcg gcg caa aac ggg gtc ccg gcg atg agc tgc ctg ggc agc tgc ctg ggt tct tgc ggt
ala ala gln asn gly val arg ala met ser ser leu gly ser ser leu gly ser ser gly
901/301
ctg gcc ggt ggg gtg gcc gcc aac ttg ggt cgg gcg gcc tgc gtc ggt tgc ttg tgc gtg
leu gly gly gly val ala ala asn leu gly arg ala ala ser val gly ser leu ser val
961/321
ccg cag gcc tgg gcc gcg gcc aac cag gca gtc acc ccg gcg gcg cgg gcg ctg ccg ctg
pro gln ala trp ala ala ala asn gln ala val thr pro ala ala arg ala leu pro leu
1021/341
acc agc ctg acc agc gcc gcg gaa aga ggg ccc ggg cag atg ctg ggc ggg ctg ccg gtg
thr ser leu thr ser ala ala glu arg gly pro gly gln met leu gly gly leu pro val
1081/361
ggg cag atg ggc gcc agg gcc ggt ggt ggg ctc agt ggt gtg ctg cgt gtt ccg ccg cga
gly gln met gly ala arg ala gly gly gly leu ser gly val leu arg val pro pro arg
1141/381
ccc tat gtg atg ccg cat tct ccg gcg gcc ggc tag
pro tyr val met pro his ser pro ala ala gly AMB

```

SEQ ID No.5R

FIGURE 5R

REPLACEMENT SHEET (RULE 26)

Seq 5P: ORF according to Cole et al. (Nature 393:537-544) and containing the sequence Rv1196

```

1/1                                31/11
tag gga cac gta atg gtg gat ttc ggg gcg tta cca ccg gag atc aac tcc gcg agg atg
AMB gly his val met val asp phe gly ala leu pro pro glu ile asn ser ala arg met
61/21                                91/31
tac gcc ggc ccg ggt tcg gcc tcg ctg gtg gcc gcg gct cag atg tgg gac agc gtg gcg
tyr ala gly pro gly ser ala ser leu val ala ala ala gln met trp asp ser val ala
121/41                                151/51
agt gac ctg ttt tcg gcc gcg tcg gcg ttt cag tcg gtg gtc tgg ggt ctg acg gtg ggg
ser asp leu phe ser ala ala ser ala phe gln ser val val trp gly leu thr val gly
181/61                                211/71
tcg tgg ata ggt tcg tcg gcg ggt ctg atg gtg gcg gcg gcc tcg ccg tat gtg gcg tgg
ser trp ile gly ser ser ala gly leu met val ala ala ala ser pro tyr val ala trp
241/81                                271/91
atg agc gtc acc gcg ggg cag gcc gag ctg acc gcc gcc cag gtc ccg gtt gct gcg gcg
met ser val thr ala gly gln ala glu leu thr ala ala gln val arg val ala ala ala
301/101                                331/111
gcc tac gag acg gcg tat ggg ctg acg gtg ccc ccg ccg gtg atc gcc gag aac cgt gct
ala tyr glu thr ala tyr gly leu thr val pro pro pro val ile ala glu asn arg ala
361/121                                391/131
gaa ctg atg att ctg ata gcg acc aac ctc ttg ggg caa aac acc ccg gcg atc gcg gtc
glu leu met ile leu ile ala thr asn leu leu gly gln asn thr pro ala ile ala val
421/141                                451/151
aac gag gcc gaa tac ggc gag atg tgg gcc caa gac gcc gcc gcg atg ttt ggc tac gcc
asn glu ala glu tyr gly glu met trp ala gln asp ala ala ala met phe gly tyr ala
481/161                                511/171
gcg gcg acg gcg acg gcg acg gcg acg ttg ctg ccg ttc gag gag gcg ccg gag atg acc
ala ala thr ala thr ala thr ala thr leu leu pro phe glu glu ala pro glu met thr
541/181                                571/191
agc gcg ggt ggg ctc ctc gag cag gcc gcc gcg gtc gag gag gcc tcc gac acc gcc gcg
ser ala gly gly leu leu glu gln ala ala ala val glu glu ala ser asp thr ala ala
601/201                                631/211
gcg aac cag ttg atg aac aat gtg ccc cag gcg ctg caa cag ctg gcc cag ccc acg cag
ala asn gln leu met asn asn val pro gln ala leu gln gln leu ala gln pro thr gln
661/221                                691/231
ggc acc acg cct tct tcc aag ctg ggt ggc ctg tgg aag acg gtc tcg ccg cat cgg tcg
gly thr thr pro ser ser lys leu gly gly leu trp lys thr val ser pro his arg ser
721/241                                751/251
ccg atc agc aac atg gtg tcg atg gcc aac aac cac atg tcg atg acc aac tcg ggt gtg
pro ile ser asn met val ser met ala asn asn his met ser met thr asn ser gly val
781/261                                811/271
tcg atg acc aac acc ttg agc tcg atg ttg aag ggc ttt gct ccg gcg gcg gcc gcc cag
ser met thr asn thr leu ser ser met leu lys gly phe ala pro ala ala ala ala gln
841/281                                871/291
gcc gtg caa acc gcg gcg caa aac ggg gtc cgg gcg atg agc tcg ctg ggc agc tcg ctg
ala val gln thr ala ala gln asn gly val arg ala met ser ser leu gly ser ser leu
901/301                                931/311
ggt tct tcg ggt ctg ggc ggt ggg gtg gcc gcc aac ttg ggt cgg gcg gcc tcg gtc ggt
gly ser ser gly leu gly gly gly val ala ala asn leu gly arg ala ala ser val gly
961/321                                991/331
tcg ttg tcg gtg ccg cag gcc tgg gcc gcg gcc aac cag gca gtc acc ccg gcg gcg ccg
ser leu ser val pro gln ala trp ala ala ala asn gln ala val thr pro ala ala arg
1021/341                                1051/351
gcg ctg ccg ctg acc agc ctg acc agc gcc gcg gaa aga ggg ccc ggg cag atg ctg ggc
ala leu pro leu thr ser leu thr ser ala ala glu arg gly pro gly gln met leu gly
1081/361 1111/371
ggg ctg ccg gtg ggg cag atg ggc gcc agg gcc ggt ggt ggg ctc agt ggt gtg ctg cgt
gly leu pro val gly gln met gly ala arg ala gly gly gly leu ser gly val leu arg
1141/381                                1171/391
gtt ccg ccg cga ccc tat gtg atg ccg cat tct ccg gcg gcc ggc tag
val pro pro arg pro tyr val met pro his ser pro ala ala gly AMB

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SEQ ID No.5P

FIGURE 5P

REPLACEMENT SHEET (RULE 26)

31/11
 GGA TCC TGA TGC AAG TGG TCC GGG ATT TGT CGG CAG CCA CCG CGG TCC CGT CGA CCA ACG
 gly ser OPA cys lys trp ser gly ile cys arg gln pro arg arg ser arg arg pro thr
 61/21
 TTG GTG CAT CCG GGC TGC GAG CAT GCA CGC ACC GAC CAG CGC GGC GAG CGC GGC TAG CTG
 leu val his pro gly cys glu his ala arg thr asp gln arg gly glu arg gly AMB leu
 121/41
 CTT GCC CAC TGT TCC TCC CTG CCG GCA CCA TGT GCG ACA AGC TTA AGC GCA GCA GTA CCG
 leu ala his cys ser ser leu pro ala pro cys ala thr ser leu ser ala ala val pro
 181/61
 GCG GTG CCT GGG CAT CCA GCA AAA CGG GGA GCT CAA GAA CGA TTC ATG AAC GAG GGG TCG
 ala val pro gly his pro ala lys arg gly ala gln glu arg phe met asn glu gly sec
 241/81
 TCA CCA ACG TCG AAA CCG ACG GTT GCC AGC CGG CCC ACG ATA TTG CGT GCT CGA GGG TCC
 ser pro thr ser lys pro thr val ala ser arg pro thr ile leu arg ala arg gly ser
 301/101
 GCT GTA CCC TCA CCG AAC GTG AGT CCC ACA CCG CGG AGG CGG GCG ACT CTG GCG TCG TTA
 ala val pro ser pro asn val ser pro thr pro arg arg arg ala thr leu ala ser leu
 361/121
 GCA GCC GAG CTC AAG GTG TCC CGC ACC ACT GTC TCG AAT GCT TTT AAC CGA CCG GAT CCA
 ala ala glu leu lys val ser arg thr thr val ser asn ala phe asn arg pro asp pro
 421/141
 GAA GGA GAA GAT C
 glu gly glu asp

SEQ ID No.6A

FIGURE 6A

32/11
 GAT CCT GAT GCA AGT GGT CCG GGA TTT GTC GGC AGC CAC GGC GGT CCC GTC GAC CAA CGT
 asp pro asp ala ser gly pro gly phe val gly ser his gly gly pro val asp gln arg
 62/21
 TGG TGC ATC CGG GCT GCG AGC ATG CAC GCA CCG ACC AGC GCG GCG AGC GCG GCT AGC TGC
 trp cys ile arg ala ala ser met his ala pro thr ser ala ala ser ala ala ser cys
 122/41
 TTG CCC ACT GTT CCT CCC TGC CGG CAC CAT GTG CGA CAA GCT TAA GCG CAG CAG TAC CGG
 leu pro thr val pro pro cys arg his his val arg gln ala OCH ala gln gln tyr arg
 182/61
 CGG TGC CTG GGC ATC CAG CAA AAC GGG GAG CTC AAG AAC GAT TCA TGA ACG AGG GGT CGT
 arg cys leu gly ile gln gln asn gly glu leu lys asn asp ser OPA thr arg gly arg
 242/81
 CAC CAA CGT CGA AAC CGA CGG TTG CCA GCC GGC CCA CGA TAT TGC GTG CTC GAG GGT CCG
 his gln arg arg asn arg arg leu pro ala gly pro arg tyr cys val leu glu gly pro
 302/101
 CTG TAC CCT CAC CGA ACG TGA GTC CCA CAC CGC GGA GGC GGG CGA CTC TGG CGT CGT TAG
 leu tyr pro his arg thr OPA val pro his arg gly gly gly arg leu trp arg arg AMB
 362/121
 CAG CCG AGC TCA AGG TGT CCC GCA CCA CTG TCT CGA ATG CTT TTA ACC GAC CGG ATC CAG
 gln pro ser ser arg cys pro ala pro leu ser arg met leu leu thr asp arg ile gln
 422/141
 AAG GAG AAG ATC
 lys glu lys ile

SEQ ID No.6B

FIGURE 6B

20/185

33/11
 ATC CTG ATG CAA GTG GTC CGG GAT TTG TCG GCA GCC ACG GCG GTC CCG TCG ACC AAC GTT
 ile leu met gln val val arg asp leu ser ala ala thr ala val pro ser thr asn val
 63/21
 GGT GCA TCC GGG CTG CGA GCA TGC ACG CAC CGA CCA GCG CGG CGA GCG CGG CTA GCT GCT
 gly ala ser gly leu arg ala cys thr his arg pro ala arg arg ala arg leu ala ala
 123/41
 TGC CCA CTG TTC CTC CCT GCC GGC ACC ATG TGC GAC AAG CTT AAG CGC AGC AGT ACC GGC
 cys pro leu phe leu pro ala gly thr met cys asp lys leu lys arg scr ser thr gly
 183/61
 GGT GCC TGG GCA TCC AGC AAA ACG GGG AGC TCA AGA ACG ATT CAT GAA CGA GGG GTC GTC
 gly ala trp ala ser ser lys thr gly ser ser arg thr ile his glu arg gly val val
 243/81
 ACC AAC GTC GAA ACC GAC GGT TGC CAG CCG GCC CAC GAT ATT GCG TGC TCG AGG GTC CGC
 thr asn val glu thr asp gly cys gln pro ala his asp ile ala cys ser arg val arg
 303/101
 TGT ACC CTC ACC GAA CGT GAG TCC CAC ACC GCG GAG GCG GGC GAC TCT GGC GTC GTT AGC
 cys thr leu thr glu arg glu ser his thr ala glu ala gly asp ser gly val val ser
 363/121
 AGC CGA GCT CAA GGT GTC CCG CAC CAC TGT CTC GAA TGC TTT TAA CCG ACC GGA TCC AGA
 ser arg ala gln gly val pro his his cys leu glu cys phe OCH pro thr gly ser arg
 423/141
 AGG AGA AGA TC
 arg arg arg

SEQ ID No.6C

FIGURE 6C

31/11
 CCG TCG GCA ACT TGG CCG CTG AGG TCG GCT TGA TCC CTG GGC CGA GGC GGG TCA GCC AAT
 pro ser ala thr trp pro leu arg ser ala OPA ser leu gly arg gly gly ser ala asn
 61/21
 AGC GGC TCC ATC GGC TTT GCT GGT AGC GGT TCG GCG GGA AGC TAG CGG CGA CGT TGT CGG
 ser gly ser ile gly phe ala gly ser gly ser ala gly ser AMB arg arg arg cys arg
 121/41
 TGG CCG GTG ATA TAT TCG GTC AGA CGG GTA TGG CCG CGG CTG AGG TGA TCT GCG ACA CGC
 trp pro val ile tyr trp val arg arg val trp arg arg leu arg OPA ser ala thr arg
 181/61
 CGC CGC GGT GCT CGA GCC AGG CTT ACG ACC AGG GAA TTT CGA AAA TGT TAT TCA GAA CAT
 arg arg gly ala arg ala arg leu thr thr arg glu phe arg lys cys tyr ser glu his
 241/81
 CTT GTA TCT CTT CTC CGT GCC ACC CCC TAG GTG TAG TGT TTT CGA GTA CCG GCA GAT CCC
 leu val ser leu leu arg ala thr pro AMB val AMB cys phe arg val pro ala asp pro
 301/101
 AGG TTC ACC AGG TCT CAC CAG ATC
 arg phe thr arg ser his gln ile

SEQ ID No.7A

FIGURE 7A

32/11
 CGT CGG CAA CTT GGC CGC TGA GGT CGG CTT GAT CCC TGG GCC GAG GCG GGT CAG CCA ATA
 arg arg gln leu gly arg OPA gly arg leu asp pro trp ala glu ala gly gln pro ile
 62/21 92/31
 GCG GCT CCA TCG GCT TTG CTG GTA GCG GTT CGG CGG GAA GCT AGC GGC GAC GTT GTC GGT
 ala ala pro ser ala leu leu val ala val arg arg glu ala ser gly asp val val gly
 122/41 152/51
 GGC CGG TGA TAT ATT GGG TCA GAC GGG TAT GGC GGC GGC TGA GGT GAT CTG CGA CAC GCC
 gly arg OPA tyr ile gly ser asp gly tyr gly gly gly OPA gly asp leu arg his ala
 182/61 212/71
 GCC GCG GTG CTC GAG CCA GGC TTA CGA CCA GGG AAT TTC GAA AAT GTT ATT CAG AAC ATC
 ala ala val leu glu pro gly leu arg pro gly asn phe glu asn val ile gln asn ile
 242/81 272/91
 TTG TAT CTC TTC TCC GTG CCA CCC CCT AGG TGT AGT GTT TTC GAG TAC CGG CAG ATC CCA
 leu tyr leu phe ser val pro pro pro arg cys ser val phe glu tyr arg gln ile pro
 302/101
 GGT TCA CCA GGT CTC ACC AGA TC
 gly ser pro gly leu thr arg

SEQ ID No.7B

FIGURE 7B

33/11
 GTC GGC AAC TTG GCC GCT GAG GTC GGC TTG ATC CCT GGG CCG AGG CGG GTC AGC CAA TAG
 val gly asn leu ala ala glu val gly leu ile pro gly pro arg arg val ser gln AMB
 63/21 93/31
 CGG CTC CAT CGG CTT TGC TGG TAG CGG TTC GGC GGG AAG CTA GCG GCG ACG TTG TCG GTG
 arg leu his arg leu cys trp AMB arg phe gly gly lys leu ala ala thr leu ser val
 123/41 153/51
 GCC GGT GAT ATA TTG GGT CAG ACG GGT ATG GCG GCG GCT GAG GTG ATC TGC GAC ACG CCG
 ala gly asp ile leu gly gln thr gly met ala ala ala glu val ile cys asp thr pro
 183/61 213/71
 CCG CGG TGC TCG AGC CAG GCT TAC GAC CAG GGA ATT TCG AAA ATG TTA TTC AGA ACA TCT
 pro arg cys ser ser gln ala tyr asp gln gly ile ser lys met leu phe arg thr ser
 243/81 273/91
 TGT ATC TCT TCT CCG TGC CAC CCC CTA GGT GTA GTG TTT TCG AGT ACC GGC AGA TCC CAG
 cys ile ser ser pro cys his pro leu gly val val phe ser ser thr gly arg ser gln
 303/101
 GTT CAC CAG GTC TCA CCA GAT C
 val his gln val ser pro asp

SEQ ID No.7C

FIGURE 7C

22/185

31/11
 CTT TGC GTG ATG TCC AAT GGC GAA AAC GAC GCC TTG TCA TCG CAA TCG TCA GCA CCG GCC
 leu cys val met ser asn gly glu asn asp ala leu ser ser gln ser ser ala pro ala
 61/21
 TAG TTT TCG CGA TGA CGC TCG TTC TGA CCG GAC TTG TGA ACG GGT TTC GGG TCG AGG CCG
 AMB phe ser arg OPA arg ser phe OPA pro asp leu OPA thr gly phe gly ser arg pro
 121/41
 AGC GAA CCG TCG ATT CCA TGG GTG TCG ACG CAT TCG TGG TCA AGG CCG GCG CGG CAG GAC
 ser glu pro ser ile pro trp val ser thr his ser trp ser arg pro ala arg gln asp
 181/61
 CGT TCC TGG GTT CGA CAC CAT TCG CCC AAA TCG ACC TGC CCC AGG TTG CTC GTG CGC CTG
 arg ser trp val arg his his ser pro lys ser thr cys pro arg leu leu val arg leu
 241/81
 GCG TCT TGG CTG CCG CCC CAC TAG CGA CTG CGC CGT CGA CGA TCC GGC AGG GCA CGT CAG
 ala ser trp leu pro pro his AMB arg leu arg arg arg arg ser gly arg ala arg gln
 301/101
 CGC GAA ACG TCA CCG CGT TCG GGG CAC CAG AGC ACG GAC CCG GCA TGC CGC GGG TCT CGG
 arg glu thr ser pro arg ser gly his gln ser thr asp pro ala cys arg gly ser arg
 361/121
 ACG GTC GGG CGC CAT CGA CGC CGG ACG AGG TCG CGG TGT CGA GCA CGC TGG GCC GAA ACC
 thr val gly arg his arg arg arg thr arg ser arg cys arg ala arg trp ala glu thr
 421/141
 TCG GCG ACG ATC
 ser ala thr ile

SEQ ID No.8A

FIGURE 8A

32/11
 TTT GCG TGA TGT CCA ATG GCG AAA ACG ACG CCT TGT CAT CGC AAT CGT CAG CAC CGG CCT
 phe ala OPA cys pro met ala lys thr thr pro cys his arg asn arg gln his arg pro
 62/21
 AGT TTT CGC GAT GAC GCT CGT TCT GAC CGG ACT TGT GAA CGG GTT TCG GGT CGA GGC CGA
 ser phe arg asp asp ala arg ser asp arg thr cys glu arg val ser gly arg gly arg
 122/41
 GCG AAC CGT CGA TTC CAT GGG TGT CGA CGC ATT CGT GGT CAA GGC CGG CGC GGC AGG ACC
 ala asn arg arg phe his gly cys arg arg ile arg gly gln gly arg arg gly arg thr
 182/61
 GTT CCT GGG TTC GAC ACC ATT CGC CCA AAT CGA CCT GCC CCA GGT TGC TCG TGC GCC TGG
 val pro gly phe asp thr ile arg pro asn arg pro ala pro gly cys ser cys ala trp
 242/81
 CGT CTT GGC TGC CGC CCC ACT AGC GAC TGC GCC GTC GAC GAT CCG GCA GGG CAC GTC AGC
 arg leu gly cys arg pro thr ser asp cys ala val asp asp pro ala gly his val ser
 302/101
 GCG AAA CGT CAC CGC GTT CGG GGC ACC AGA GCA CGG ACC CGG CAT GCC GCG GGT CTC GGA
 ala lys arg his arg val arg gly thr arg ala arg thr arg his ala ala gly leu gly
 362/121
 CGG TCG GGC GCC ATC GAC GCC GGA CGA GGT CGC GGT GTC GAG CAC GCT GGG CCG AAA CCT
 arg ser gly ala ile asp ala gly arg gly arg gly val glu his ala gly pro lys pro
 422/141
 CGG CGA CGA TC
 arg arg arg

SEQ ID No.8B

FIGURE 8B

REPLACEMENT SHEET (RULE 26)

23/185

33/11
 TTG CGT GAT GTC CAA TGG CGA AAA CGA CGC CTT GTC ATC GCA ATC GTC AGC ACC GGC CTA
 leu arg asp val gln trp arg lys arg arg leu val ile ala ile val ser thr gly leu
 63/21
 GTT TTC GCG ATG ACG CTC GTT CTG ACC GGA CTT GTG AAC GGG TTT CGG GTC GAG GCC GAG
 val phe ala met thr leu val leu thr gly leu val asn gly phe arg val glu ala glu
 123/41
 CGA ACC GTC GAT TCC ATG GGT GTC GAC GCA TTC GTG GTC AAG GCC GGC GCG GCA GGA CCG
 arg thr val asp ser met gly val asp ala phe val val lys ala gly ala ala gly pro
 183/61
 TTC CTG GGT TCG ACA CCA TTC GCC CAA ATC GAC CTG CCC CAG GTT GCT CGT GCG CCT GGC
 phe leu gly ser thr pro phe ala gln ile asp leu pro gln val ala arg ala pro gly
 243/81
 GTC TTG GCT GCC GCC CCA CTA GCG ACT GCG CCG TCG ACG ATC CGG CAG GGC ACG TCA GCG
 val leu ala ala ala pro leu ala thr ala pro ser thr ile arg gln gly thr ser ala
 303/101
 CGA AAC GTC ACC GCG TTC GGG GCA CCA GAG CAC GGA CCC GGC ATG CCG CGG GTC TCG GAC
 arg asn val thr ala phe gly ala pro glu his gly pro gly met pro arg val ser asp
 363/121
 GGT CGG GCG CCA TCG ACG CCG GAC GAG GTC GCG GTG TCG AGC ACG CTG GGC CGA AAC CTC
 gly arg ala pro ser thr pro asp glu val ala val ser ser thr leu gly arg asn leu
 423/141
 GGC GAC GAT C
 gly asp asp

SEQ ID No.8C

FIGURE 8C

part of the nucleotide sequence of seq8A

1/1
 CAG GTT GCT CGT GCG CCT GGC GTC TTG GCT GCC GCC CCA CTA GCG ACT GCG CCG TCG ACG
 gln val ala arg ala pro gly val leu ala ala ala pro leu ala thr ala pro ser thr
 61/21
 ATC CGG CAG GGC ACG TCA GCG CGA AAC GTC ACC GCG TTC GGG GCA CCA GAG CAC GGA CCC
 ile arg gln gly thr ser ala arg asn val thr ala phe gly ala pro glu his gly pro
 121/41
 GGC ATG CCG CGG GTC TCG GAC GGT CGG GCG CCA TCG ACG CCG GAC GAG GTC GCG GTG TCG
 gly met pro arg val ser asp gly arg ala pro ser thr pro asp glu val ala val ser
 181/61
 AGC ACG CTG GGC CGA AAC CTC GGC GAC GAT C
 ser thr leu gly arg asn leu gly asp asp

SEQ ID No.8A'

FIGURE 8A'

sequence Rv2563 predicted by Cole et al. (Nature 393:537-544) and containing seq8A'

```

atg
met
121/41
ctt ttt gcg gct ttg cgt gat gtc caa tgg cga aaa cga cgc ctt gtc atc gca atc gtc
leu phe ala ala leu arg asp val gln trp arg lys arg arg leu val ile ala ile val
181/61
agc acc ggc cta gtt ttc gcg atg acg ctc gtt ctg acc gga ctt gtg aac ggg ttt cgg
ser thr gly leu val phe ala met thr leu val leu thr gly leu val asn gly phe arg
241/81
gtc gag gcc gag cga acc gtc gat tcc atg ggt gtc gac gca ttc gtg gtc aag gcc ggc
val glu ala glu arg thr val asp ser met gly val asp ala phe val val lys ala gly
301/101
gcg gca gga cgg ttc ctg ggt tcg aca cca ttc gcc caa atc gac ctg ccc cag gtt gct
ala ala gly pro phe leu gly ser thr pro phe ala gln ile asp leu pro gln val ala
361/121
cgt gcg cct ggc gtc ttg gct gcc gcc cca cta gcg act gcg ccg tcg acg atc cgg cag
arg ala pro gly val leu ala ala ala pro leu ala thr ala pro ser thr ile arg gln
421/141
ggc acg tca gcg cga aac gtc acc gcg ttc ggg gca cca gag cac gga ccc ggc atg ccg
gly thr ser ala arg asn val thr ala phe gly ala pro glu his gly pro gly met pro
481/161
cgg gtc tcg gac ggt cgg gcg cca tcg acg ccg gac gag gtc gcg gtg tcg agc acg ctg
arg val ser asp gly arg ala pro ser thr pro asp glu val ala val ser ser thr leu
541/181
ggc cga aac ctc ggc gac gat ctg caa gtg ggt gcg cgc act ttg cgg atc gtc ggc atc
gly arg asn leu gly asp asp leu gln val gly ala arg thr leu arg ile val gly ile
601/201
gtg ccc gag tca acc gcg ctg gca aag att ccc aac atc ttc ctg acc acc gaa ggc cta
val pro glu ser thr ala leu ala lys ile pro asn ile phe leu thr thr glu gly leu
661/221
cag cag ttg gca tac aac gga cag ccg aca atc agt tcg atc ggg atc gac ggg atg ccc
gln gln leu ala tyr asn gly gln pro thr ile ser ser ile gly ile asp gly met pro
721/241
cga cag ctc ccg gac ggc tat cag acc gtc aat cga gcg gat gct gtc agc gat ctg atg
arg gln leu pro asp gly tyr gln thr val asn arg ala asp ala val ser asp leu met
781/261
cgc ccg ttg aag gtc gcg gtg gat gcg atc acg gtt gtg gcg gtc ttg ctg tgg atc gtt
arg pro leu lys val ala val asp ala ile thr val val ala val leu leu trp ile val
841/281
gcg gcg ttg atc gtc ggc tcg gtg gtc tac ctc tct gcg ttg gag ccg ctg cgt gac ttt
ala ala leu ile val gly ser val val tyr leu ser ala leu glu arg leu arg asp phe
901/301
gcg gtg ttc aag gcg atc ggc gtg ccg acg cgc tcg att ctg gcc ggg ctg gcg ctg cag
ala val phe lys ala ile gly val pro thr arg ser ile leu ala gly leu ala leu gln
961/321
gcg gtc gtc gtc gcg ctg ctc gcg gcg gtg gtt ggc ggc atc ctt tcg ctg ctg ttg gcg
ala val val val ala leu leu ala ala val val gly gly ile leu ser leu leu leu ala
1021/341
ccg ttg ttc ccg atg act gtc gtg gta ccc ctg agt gcc ttc gtg gcg cta ccg gcg atc
pro leu phe pro met thr val val val pro leu ser ala phe val ala leu pro ala ile
1081/361
gcg act gtg atc ggt ctg ctg gcc agc gtc gca gga ctg ccg cgc gtg gtg gcg atc gat
ala thr val ile gly leu leu ala ser val ala gly leu arg arg val val ala ile asp
1141/381
ccg gca cta gcg ttc gga ggt ccc tag
pro ala leu ala phe gly gly pro AMB

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SEQ ID No.8D

FIGURE 8D

REPLACEMENT SHEET (RULE 26)

ORF predicted by Cole et al. (Nature 393:537-544) and containing Rv2563

1/1 31/11
tag gtt tca aga agg cct gtg cag gtt tcc gca gcc tgg gcc gcg gcg cca ccg aag agc
AMB val ser arg arg pro val gln val ser ala ala trp ala ala ala pro pro lys ser
61/21 91/31
ccg ccg aaa tgg gct aat cgg gtt cgc ttg gct cga tcg ccg atg atc tcg acc gcc acg
pro pro lys trp ala asn arg val arg leu ala arg ser pro met ile ser thr ala thr
121/41 151/51
acc gac ccc ctc acc tcg gtc gaa cct cgg cga acc aac gcg gca acg cca gcc cat gat
thr asp pro leu thr ser val glu pro arg arg thr asn ala ala thr pro ala his asp
181/61 211/71
cat ttg att ggg tcc acg gaa gca ggt agc ttc cgt cgc atg ctt ttt gcg gct ttg cgt
his leu ile gly ser thr glu ala gly ser phe arg arg met leu phe ala ala leu arg
241/81 271/91
gat gtc caa tgg cga aaa cga cgc ctt gtc atc gca atc gtc agc acc ggc cta gtt ttc
asp val gln trp arg lys arg arg leu val ile ala ile val ser thr gly leu val phe
301/101 331/111
gcg atg acg ctc gtt ctg acc gga ctt gtg aac ggg ttt cgg gtc gag gcc gag cga acc
ala met thr leu val leu thr gly leu val asn gly phe arg val glu ala glu arg thr
361/121 391/131
gtc gat tcc atg ggt gtc gac gca ttc gtg gtc aag gcc ggc gcg gca gga ccg ttc ctg
val asp ser met gly val asp ala phe val val lys ala gly ala ala gly pro phe leu
421/141 451/151
ggt tcg aca cca ttc gcc caa atc gac ctg ccc cag gtt gct cgt gcg cct ggc gtc ttg
gly ser thr pro phe ala gln ile asp leu pro gln val ala arg ala pro gly val leu
481/161 511/171
gct gcc gcc cca cta gcg act gcg ccg tcg acg atc cgg cag ggc acg tca gcg cga aac
ala ala ala pro leu ala thr ala pro ser thr ile arg gln gly thr ser ala arg asn
541/181 571/191
gtc acc gcg ttc ggg gca cca gag cac gga ccc ggc atg ccg cgg gtc tcg gac ggt cgg
val thr ala phe gly ala pro glu his gly pro gly met pro arg val ser asp gly arg
601/201 631/211
gcg cca tcg acg ccg gac gag gtc gcg gtg tcg agc acg ctg ggc cga aac ctc ggc gac
ala pro ser thr pro asp glu val ala val ser ser thr leu gly arg asn leu gly asp
661/221 691/231
gat ctg caa gtg ggt gcg cgc act ttg cgg atc gtc ggc atc gtg ccc gag tca acc gcg
asp leu gln val gly ala arg thr leu arg ile val gly ile val pro glu ser thr ala
721/241 751/251
ctg gca aag att ccc aac atc ttc ctg acc acc gaa ggc cta cag cag ttg gca tac aac
leu ala lys ile pro asn ile phe leu thr thr glu gly leu gln gln leu ala tyr asn
781/261 811/271
gga cag ccg aca atc agt tcg atc ggg atc gac ggg atg ccc cga cag ctc ccg gac ggc
gly gln pro thr ile ser ser ile gly ile asp gly met pro arg gln leu pro asp gly
841/281 871/291
tat cag acc gtc aat cga gcg gat gct gtc agc gat ctg atg cgc ccg ttg aag gtc gcg
tyr gln thr val asn arg ala asp ala val ser asp leu met arg pro leu lys val ala
901/301 931/311
gtg gat gcg atc acg gtt gtg gcg gtc ttg ctg tgg atc gtt gcg gcg ttg atc gtc ggc
val asp ala ile thr val val ala val leu leu trp ile val ala ala leu ile val gly
961/321 991/331
tcg gtg gtc tac ctc tct gcg ttg gag ccg ctg cgt gac ttt gcg gtg ttc aag gcg atc
ser val val tyr leu ser ala leu glu arg leu arg asp phe ala val phe lys ala ile
1021/341 1051/351
ggc gtg ccg acg cgc tcg att ctg gcc ggg ctg gcg ctg cag gcg gtc gtc gtc gcg ctg
gly val pro thr arg ser ile leu ala gly leu ala leu gln ala val val val ala leu
1081/361 1111/371
ctc gcg gcg gtg gtt ggc ggc atc ctt tcg ctg ctg ttg gcg ccg ttg ttc ccg atg act
leu ala ala val val gly gly ile leu ser leu leu leu ala pro leu phe pro met thr
1141/381 1171/391
gtc gtg gta ccc ctg agt gcc ttc gtg gcg cta ccg gcg atc gcg act gtg atc ggt ctg
val val val pro leu ser ala phe val ala leu pro ala ile ala thr val ile gly leu
1201/401 1231/411
ctg gcc agc gtc gca gga ctg ccg cgc gtg gtg gcg atc gat ccg gca cta gcg ttc gga
leu ala ser val ala gly leu arg arg val val ala ile asp pro ala leu ala phe gly
1261/421
ggt ccc tag
gly pro AMB

SEQ ID No.8F

FIGURE 8F

sequence of Rv0072 predicted by Cole et al. (Nature 393:537-544) and exhibiting more than 77% similarity with Seq8D'

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1/1
atg ctc ttc gcg gcc ctg cgt gac atg caa tgg aga aag cgc cgc ctg gtc atc acg atc
Met leu phe ala ala leu arg asp met gln trp arg lys arg arg leu val ile thr ile
61/21
atc agc acc ggg ctg atc ttc ggg atg acg ctt gtt ttg acc gga ctc gcg aac ggc ttc
ile ser thr gly leu ile phe gly met thr leu val leu thr gly leu ala asn gly phe
121/41
cgg gtg gag gcc cgg cac acc gtc gat tcc atg ggt gtc gat gta ttc gtc gtc aga tcc
arg val glu ala arg his thr val asp ser met gly val asp val phe val val arg ser
181/61
ggc gct gct gga cct ttt ctg ggt tca ata ccg ttt ccc gat gtt gac ctg gcc cga gtg
gly ala ala gly pro phe leu gly ser ile pro phe pro asp val asp leu ala arg val
241/81
gcc gct gaa ccc ggt gtc atg gcc gcg gcc ccg ttg ggc agc gtg ggg acg atc atg aaa
ala ala glu pro gly val met ala ala ala pro leu gly ser val gly thr ile met lys
301/101
gaa ggc acg tcg acg cga aac gtc acg gtc ttc ggc gcg ccc gag cac gga cct ggc atg
glu gly thr ser thr arg asn val thr val phe gly ala pro glu his gly pro gly met
361/121
cca cgg gtc tca gag ggt cgg tca ccg tcg aaa ccg gac gaa gtc gcg gca tcg agc acg
pro arg val ser glu gly arg ser pro ser lys pro asp glu val ala ala ser ser thr
421/141
atg ggc cga cac ctc ggt gac act gtc gag gtc ggc gcg cgc aga ttg cgg gtc gtt ggc
met gly arg his leu gly asp thr val glu val gly ala arg arg leu arg val val gly
481/161
att gtg ccg aat tcc acc gcg ctg gcc aag atc ccc aat gtc ttc ctc acg acc gag ggc
ile val pro asn ser thr ala leu ala lys ile pro asn val phe leu thr thr glu gly
541/181
tta cag aaa ttg gcg tac aac ggg cag ccg aat atc acg tcc atc ggg atc ata ggt atg
leu gln lys leu ala tyr asn gly gln pro asn ile thr ser ile gly ile ile gly met
601/201
ccc cga cag ctg ccg gag ggt tac cag act ttc gat ccg gtg ggc gct gtc aat gat ttg
pro arg gln leu pro glu gly tyr gln thr phe asp arg val gly ala val asn asp leu
661/221
gtg cgc cca ttg aag gtc gca gtg aat tcg atc tcg atc gtg gct gtt ttg ctg tgg att
val arg pro leu lys val ala val asn ser ile ser ile val ala val leu leu trp ile
721/241
gtg gcg gtg ctg atc gtc ggc tcg gtg gtg tac ctt tcg gct ctt gag cgg cta cgt gac
val ala val leu ile val gly ser val val tyr leu ser ala leu glu arg leu arg asp
781/261
ttc gcg gtg ttc aag gcg att ggc acg cca acg cgc tcg att atg gcc ggg ctc gca tta
phe ala val phe lys ala ile gly thr pro thr arg ser ile met ala gly leu ala leu
841/281
cag gcg ctg gtc att gcg ttg ctt gcg gcg gtg gtg ggc gtc gtc ctg gcg cag gtg ttg
gln ala leu val ile ala leu leu ala ala val val gly val val leu ala gln val leu
901/301
gca cca ctg ttt ccg atg att gtc gcg gta ccc gtc ggt gct tac ctg gcg cta ccg gtg
ala pro leu phe pro met ile val ala val pro val gly ala tyr leu ala leu pro val
961/321
gcc gcg atc gtc atc ggt ctg ttc gct agt gtt gcc gga ttg aag cgc gtg gtg acg gtc
ala ala ile val ile gly leu phe ala ser val ala gly leu lys arg val val thr val
1021/341
gat ccc gcg cag gcg ttc gga ggt ccc tag
asp pro ala gln ala phe gly gly pro AMB

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SEQ ID No.8G

FIGURE 8G

REPLACEMENT SHEET (RULE 26)

Seq8H : ORF predicted by Cole et al. (Nature 393:537-544) and containing seq8G

1/1	31/11
tag cct ctg gga atg ctc ttc gcg gcc ctg	cgt gac atg caa tgg aga aag cgc cgc ctg
AMB pro leu gly met leu phe ala ala leu	arg asp met gln trp arg lys arg arg leu
61/21	91/31
gtc atc acg atc atc agc acc ggg ctg atc	ttc ggg atg acg ctt gtt ttg acc gga ctc
val ile thr ile ile ser thr gly leu ile	phe gly met thr leu val leu thr gly leu
121/41	151/51
gcg aac ggc ttc cgg gtg gag gcc cgg cac	acc gtc gat tcc atg ggt gtc gat gta ttc
ala asn gly phe arg val glu ala arg his	thr val asp ser met gly val asp val phe
181/61	211/71
gtc gtc aga tcc ggc gct gct gga cct ttt	ctg ggt tca ata ccg ttt ccc gat gtt gac
val val arg ser gly ala ala gly pro phe	leu gly ser ile pro phe pro asp val asp
241/81	271/91
ctg gcc cga gtg gcc gct gaa ccc ggt gtc	atg gcc gcg gcc ccg ttg ggc agc gtg ggg
leu ala arg val ala ala glu pro gly val	met ala ala ala pro leu gly ser val gly
301/101	331/111
acg atc atg aaa gaa ggc acg tcg acg cga	aac gtc acg gtc ttc ggc gcg ccc gag cac
thr ile met lys glu gly thr ser thr arg	asn val thr val phe gly ala pro glu his
361/121	391/131
gga cct ggc atg cca cgg gtc tca gag ggt	cgg tca ccg tcg aaa ccg gac gaa gtc gcg
gly pro gly met pro arg val ser glu gly	arg ser pro ser lys pro asp glu val ala
421/141	451/151
gca tcg agc acg atg ggc cga cac ctc ggt	gac act gtc gag gtc ggc gcg cgc aga ttg
ala ser ser thr met gly arg his leu gly	asp thr val glu val gly ala arg arg leu
481/161	511/171
cgg gtc gtt ggc att gtg ccg aat tcc acc	gcg ctg gcc aag atc ccc aat gtc ttc ctc
arg val val gly ile val pro asn ser thr	ala leu ala lys ile pro asn val phe leu
541/181	571/191
acg acc gag ggc tta cag aaa ttg gcg tac	aac ggg cag ccg aat atc acg tcc atc ggg
thr thr glu gly leu gln lys leu ala tyr	asn gly gln pro asn ile thr ser ile gly
601/201	631/211
atc ata ggt atg ccc cga cag ctg ccg gag	ggt tac cag act ttc gat ccg gtg ggc gct
ile ile gly met pro arg gln leu pro glu	gly tyr gln thr phe asp arg val gly ala
661/221	691/231
gtc aat gat ttg gtg cgc cca ttg aag gtc	gca gtg aat tcg atc tcg atc gtg gct gtt
val asn asp leu val arg pro leu lys val	ala val asn ser ile ser ile val ala val
721/241	751/251
ttg ctg tgg att gtg gcg gtg ctg atc gtc	ggc tcg gtg gtg tac ctt tcg gct ctt gag
leu leu trp ile val ala val leu ile val	gly ser val val tyr leu ser ala leu glu
781/261	811/271
cgg cta cgt gac ttc gcg gtg ttc aag gcg	att ggc acg cca acg cgc tcg att atg gcc
arg leu arg asp phe ala val phe lys ala	ile gly thr pro thr arg ser ile met ala
841/281	871/291
ggg ctc gca tta cag gcg ctg gtc att gcg	ttg ctt gcg gcg gtg gtg ggc gtc gtc ctg
gly leu ala leu gln ala leu val ile ala	leu leu ala ala val val gly val val leu
901/301	931/311
gcg cag gtg ttg gca cca ctg ttt ccg atg	att gtc gcg gta ccc gtc ggt gct tac ctg
ala gln val leu ala pro leu phe pro met	ile val ala val pro val gly ala tyr leu
961/321	991/331
gcg cta ccg gtg gcc gcg atc gtc atc ggt	ctg ttc gct agt gtt gcc gga ttg aag cgc
ala leu pro val ala ala ile val ile gly	leu phe ala ser val ala gly leu lys arg
1021/341	1051/351
gtg gtg acg gtc gat ccc gcg cag gcg ttc	gga ggt ccc tag
val val thr val asp pro ala gln ala phe	gly gly pro AMB

SEQ ID No.8H

FIGURE 8H

REPLACEMENT SHEET (RULE 26)

31/11
 CGA GGC CGA GCG AAC CGT CGA TTC CAT GGG TGT CGA CGC ATT CGT GGT CAA GGC CGG CGC
 arg gly arg ala asn arg arg phe his gly cys arg arg ile arg gly gln gly arg arg
 61/21 91/31
 GGC AGG ACC GTT CCT GGG TTC GAC ACC ATT CGC CCA AAT CGA CCT GCC CCA GGT TGC TCG
 gly arg thr val pro gly phe asp thr ile arg pro asn arg pro ala pro gly cys ser
 121/41 151/51
 TGC GCC TGG CGT CTT GGC TGC CGC CCC ACT AGC GAC TGC GCC GTC GAC GAT CCG GCA GGG
 cys ala trp arg leu gly cys arg pro thr ser asp cys ala val asp asp pro ala gly
 181/61 211/71
 CAC GTC AGC GCG AAA CGT CAC CGC GTT CGG GGC ACC AGA GCA CGG ACC CGG CAT GCC GCG
 his val ser ala lys arg his arg val arg gly thr arg ala arg thr arg his ala ala
 241/81 271/91
 GGT CTC GGA CGG TCG GGC GCC ATC GAC GCC GGA CGA GGT CGC GGT GTC GAG CAC GCT GGG
 gly leu gly arg ser gly ala ile asp ala gly arg gly arg gly val glu his ala gly
 301/101
 CCG AAA CCT CGG CGA CGA TC
 pro lys pro arg arg arg

SEQ ID No.9A

FIGURE 9A

32/11
 GAG GCC GAG CGA ACC GTC GAT TCC ATG GGT GTC GAC GCA TTC GTG GTC AAG GCC GGC GCG
 glu ala glu arg thr val asp ser met gly val asp ala phe val val lys ala gly ala
 62/21 92/31
 GCA GGA CCG TTC CTG GGT TCG ACA CCA TTC GCC CAA ATC GAC CTG CCC GAG GTT GCT CGT
 ala gly pro phe leu gly ser thr pro phe ala gln ile asp leu pro gln val ala arg
 122/41 152/51
 GCG CCT GGC GTC TTG GCT GCC GCC CCA CTA GCG ACT GCG CCG TCG ACG ATC CGG CAG GGC
 ala pro gly val leu ala ala ala pro leu ala thr ala pro ser thr ile arg gln gly
 182/61 212/71
 ACG TCA GCG CGA AAC GTC ACC GCG TTC GGG GCA CCA GAG CAC GGA CCC GGC ATG CCG CGG
 thr ser ala arg asn val thr ala phe gly ala pro gly his gly pro gly met pro arg
 242/81 272/91
 GTC TCG GAC GGT CGG GCG CCA TCG ACG CCG GAC GAG GTC GCG GTG TCG AGC ACG CTG GGC
 val ser asp gly arg ala pro ser thr pro asp glu val ala val ser ser thr leu gly
 302/101
 CGA AAC CTC GGC GAC GAT C
 arg asn leu gly asp asp

SEQ ID No.9B

FIGURE 9B

33/11
 AGG CCG AGC GAA CCG TCG ATT CCA TGG GTG TCG ACG CAT TCG TGG TCA AGG CCG GCG CGG
 arg pro ser glu pro ser ile pro trp val ser thr his ser trp ser arg pro ala arg
 63/21
 CAG GAC CGT TCC TGG GTT CGA CAC CAT TCG CCC AAA TCG ACC TGC CCC AGG TTG CTC GTG
 gln asp arg ser trp val arg his his ser pro lys ser thr cys pro arg leu leu val
 123/41
 CGC CTG GCG TCT TGG CTG CCG CCC CAC TAG CGA CTG CGC CGT CGA CGA TCC GGC AGG GCA
 arg leu ala ser trp leu pro pro his AMB arg leu arg arg arg arg ser gly arg ala
 183/61
 CGT CAG CGC GAA ACG TCA CCG CGT TCG GGG CAC CAG AGC ACG GAC CCG GCA TGC CGC GGG
 arg gln arg glu thr ser pro arg ser gly his gln ser thr asp pro ala cys arg gly
 243/81
 TCT CGG ACG GTC GGG CGC CAT CGA CGC CGG ACG AGG TCG CGG TGT CGA GCA CGC TGG GCC
 ser arg thr val gly arg his arg arg arg thr arg ser arg cys arg ala arg trp ala
 303/101
 GAA ACC TCG GCG ACG ATC
 glu thr.ser ala thr ile

SEQ ID No.9C

FIGURE 9C

31/11
 TTA ACG ACT CAG ACG GAA ACG CTT GAA CCG CGA GGT CGC TCC GGA CAC CAA TTT GAC TCG
 leu thr thr gln thr glu thr leu glu pro arg gly arg ser gly his gln phe asp ser
 61/21
 GCT CTT TGG CAA TTG AAG GTG AGC TGC GAG CAG CCG GGT GAC CGC ATC GTT GGC CTT GCC
 ala leu trp gln leu lys val ser cys glu gln pro gly asp arg ile val gly leu ala
 121/41
 ATC AAT CGC CGG CTC GCG GAC GTA GAT AAT CAG CTC ACC GTT GGG ACC GAC CTC GAC CAG
 ile asn arg arg leu ala asp val asp asn gln leu thr val gly thr asp leu asp gln
 181/61
 GGG TCC TTT GTG ACT GCC GGG CTT GAC GCG GAC GAC CAC AGA GTC GGT CAT CGC CTA AGG
 gly ser phe val thr ala gly leu asp ala asp asp his arg val gly his arg leu arg
 241/81
 CTA CCG TTC TGA CCT GGG GCT GCG TGG GCG CCG ACG ACG TGA GGC ACG TCA TGT CTC AGC
 leu pro phe OPA pro gly ala ala trp ala pro thr thr OPA gly thr ser cys leu ser
 301/101
 GGC CCA CCG CCA CCT CGG TCG CCG GCA GTA TGT CAG CAT GTG CAG ATG ACT CCA CGC AGC
 gly pro pro pro pro arg ser pro ala val cys gln his val gln met thr pro arg ser
 361/121
 CTT GTT CGC ATC GTT GGT GTC GTG GTT GCG ACG ACC TTG GCG CTG GTG AGC GCA CCC GCC
 leu val arg ile val gly val val val ala thr thr leu ala leu val ser ala pro ala
 421/141
 GGC GGT CGT GCC GCG CAT GCG GAT C
 gly gly arg ala ala his ala asp

SEQ ID No.10A

FIGURE 10A

31/185

32/11
TAA CGA CTC AGA CGG AAA CGC TTG AAC CGC GAG GTC GCT CCG GAC ACC AAT TTG ACT CGG
OCH arg leu arg arg lys arg leu asn arg glu val ala pro asp thr asn leu thr arg
62/21
CTC TTT GGC AAT TGA AGG TGA GCT GCG AGC AGC CGG GTG ACC GCA TCG TTG GCC TTG CCA
leu phe gly asn OPA arg OPA ala ala ser ser arg val thr ala ser leu ala leu pro
122/41
TCA ATC GCC GGC TCG CGG ACG TAG ATA ATC AGC TCA CCG TTG GGA CCG ACC TCG ACC AGG
ser ile ala gly ser arg thr AMB ile ile ser ser pro leu gly pro thr ser thr arg
182/61
GGT CCT TTG TGA CTG CCG GGC TTG ACG CGG ACG ACC ACA GAG TCG GTC ATC GCC TAA GGC
gly pro leu OPA leu pro gly leu thr arg thr thr thr glu ser val ile ala OCH gly
242/81
TAC CGT TCT GAC CTG GGG CTG CGT GGG CGC CGA CGA CGT GAG GCA CGT CAT GTC TCA GCG
tyr arg ser asp leu gly leu arg gly arg arg arg arg glu ala arg his val ser ala
302/101
GCC CAC CGC GAC CTC GGT CGC CGG CAG TAT GTC AGC ATG TGC AGA TGA CTC CAC GCA GCC
ala his arg his leu gly arg arg gln tyr val ser met cys arg OPA leu his ala ala
362/121
TTG TTC GCA TCG TTG GTG TCG TGG TTG CGA CGA CCT TGG CGC TGG TGA GCG CAC CCG CCG
leu phe ala ser leu val ser trp leu arg arg pro trp arg trp OPA ala his pro pro
422/141
GCG GTC GTG CCG CGC ATG CGG ATC
ala val val pro arg met arg ile

SEQ ID No.10B

FIGURE 10B

33/11
AAC GAC TCA GAC GGA AAC GCT TGA ACC GCG AGG TCG CTC CGG ACA CCA ATT TGA CTC GGC
asn asp ser asp gly asn ala OPA thr ala arg ser leu arg thr pro ile OPA leu gly
63/21
TCT TTG GCA ATT GAA GGT GAG CTG CGA GCA GCC GGG TGA CCG CAT CGT TGG CCT TGC CAT
ser leu ala ile glu gly glu leu arg ala ala gly OPA pro his arg trp pro cys his
123/41
CAA TCG CCG GCT CGC GGA CGT AGA TAA TCA GCT CAC CGT TGG GAC CGA CCT CGA CCA GGG
gln ser pro ala arg gly arg arg OCH ser ala his arg trp asp arg pro arg pro gly
183/61
GTC CTT TGT GAC TGC CGG GCT TGA CGC GGA CGA CCA CAG AGT CGG TCA TCG CCT AAG GCT
val leu cys asp cys arg ala OPA arg gly arg pro gln ser arg ser ser pro lys ala
243/81
ACC GTT CTG ACC TGG GGC TGC GTG GGC GCC GAC GAC GTG AGG CAC GTC ATG TCT CAG CGG
thr val leu thr trp gly cys val gly ala asp asp val arg his val met ser gln arg
303/101
CCC ACC GCC ACC TCG GTC GCC GGC AGT ATG TCA GCA TGT GCA GAT GAC TCC ACG CAG CCT
pro thr ala thr ser val ala gly ser met ser ala cys ala asp asp ser thr gln pro
363/121
TGT TCG CAT CGT TGG TGT CGT GGT TGC GAC GAC CTT GGC GCT GGT GAG CGC ACC CGC CGG
cys ser his arg trp cys arg gly cys asp asp leu gly ala gly glu arg thr arg arg
423/141
CGG TCG TGC CGC GCA TGC GGA TC
arg ser cys arg ala cys gly

SEQ ID No.10C

FIGURE 10C

REPLACEMENT SHEET (RULE 26)

REPLACEMENT SHEET (RULE 26)

32/185

31/11
 CCC GAA GAG GTC CCC CGT TTT GTT AAT TTT TAA AAA ATT TGT GTC ACA AAC CGG GGT ACC
 pro glu glu val pro arg phe val asp phe OCH lys ile cys val thr lys arg gly thr
 61/21
 AAG GCA TAA AAC CTA GTA CCT GGG GCG GCG GAT TCA ACG AAA ACC GAG TGG GGG TAG TCA
 lys ala OCH asn leu val pro gly ala ala asp ser thr lys thr glu trp gly AMB ser
 121/41
 GGG GCG TGC ATT CCG ACG ACC CTG TAC GAC CCG CTG GTG GCA ACG CCG ATG AGT GCG CCG
 gly ala cys ile pro thr thr leu tyr asp pro leu val ala thr pro met ser ala pro
 181/61
 ACG AAG GCC GAG CGA CGG GCT GCC GGC GCT GAC CGC CGC GGA AGC CGC CGA GTG CAT GGT
 thr lys ala glu arg arg ala ala gly ala asp arg arg gly ser arg arg val asp gly
 241/81
 CAC CAC CGC CCG CAC CCG ACC GGT ACG GAT CGC GCC TCG GGT TAC CGT CGC CGT CAA CGC
 his his arg pro his pro thr gly thr asp arg ala ser gly tyr arg arg arg gln arg
 301/101
 GCT GGA CAG CAT CGG TCC CCG CTG GGT CAA TGC ACT CAT GCA GCG CCG CAA CGA ACA GCT
 ala gly gln his arg ser pro leu gly gln cys thr his ala ala pro gln arg thr ala
 361/121
 CAA CCC TTG AAC CGG GTC CCG GCC TGC CGA CCC TCG GCC GCC GGC GTG CCG CTA CGT GAT
 gln pro leu asn arg val pro ala cys arg pro ser ala ala gly val pro leu arg asp
 421/141
 AGA CAC AGG GCC ATG GAA ATC CTG GCC AGC CGG ATG CTA CTT CGG CCG GCG GAC TAT CAG
 arg his arg ala met glu ile leu ala ser arg met leu leu arg pro ala asp tyr gln
 481/161
 CGG TCG CTG AGC TTC TAC CGT GAC CAG ATC
 arg ser leu ser phe tyr arg asp gln ile

SEQ ID No.11A

FIGURE 11A

32/11
 CCG AAG AGG TCC CCC GTT TTG TTA ATT TTT AAA AAA TTT GTG TCA CAA AGC GGG GTA CCA
 pro lys arg ser pro val leu leu ile phe lys lys phe val ser gln ser gly val pro
 62/21
 AGG CAT AAA ACC TAG TAC CTG GGG CGG CGG ATT CAA CGA AAA CCG AGT GGG GGT AGT CAG
 arg his lys thr AMB tyr leu gly arg arg ile gln arg lys pro ser gly gly ser gln
 122/41
 GGG CGT GCA TTC CGA CGA CCC TGT ACG ACC CGC TGG TGG CAA CGC CGA TGA GTG CCC CGA
 gly arg ala phe arg arg pro cys thr thr arg trp trp gin arg arg OPA val arg arg
 182/61
 CGA AGG ccG AGC GAC GGG CTG CCG GCG CTG ACC GCC GCG GAA GCC GCC GAG TGG ATG GTC
 arg arg pro ser asp gly leu pro ala leu thr ala ala glu ala ala glu trp met val
 242/81
 ACC ACC GCC CGC ACC CGA CCG GTA CGG ATC GCG CCT CGG GTT ACC GTC GCC GTC ACC GCG
 thr thr ala arg thr arg pro val arg ile ala pro arg val thr val ala val asn ala
 302/101
 CTG GAC AGC ATC GGT CCC CGC TGG GTC AAT GCA CTC ATG CAG CGC CGC AAC GAA CAG CTC
 leu asp ser ile gly pro arg trp val asn ala leu met gln arg arg asn glu gln leu
 362/121
 AAC CCT TGA ACC GGG TCC CGG CCT GCC GAC CCT CGG CCG CCG GCG TGC CGC TAC GTG ATA
 asn pro OPA thr gly ser arg pro ala asp pro arg pro pro ala cys arg tyr val ile
 422/141
 GAC ACA GGG CCA TGG AAA TCC TGG CCA GCC GGA TGC TAC TTC GCC CGG CGG ACT ATC AGC
 asp thr gly pro trp lys ser trp pro ala gly cys tyr phe gly arg arg thr ile ser
 482/161
 GGT CGC TGA GCT TCT ACC GTG ACC AGA TC
 gly arg OPA ala ser thr val thr arg

SEQ ID No.11B

FIGURE 11B

33/11
 CGA AGA GGT CCC CCG TTT TGT TAA TTT TTA AAA AAT TTG TGT CAC AAA GCG GGG TAC CAA
 arg arg gly pro pro phe cys OCH phe leu lys asn leu cys his lys ala gly tyr gln
 63/21
 GGC ATA AAA CCT AGT ACC TGG GGC GGC GGA TTC AAC GAA AAC CGA GTG GGG GTA GTC AGG
 gly ile lys pro ser thr trp gly gly gly phe asn glu asn arg val gly val val arg
 123/41
 GGC GTG CAT TCC GAC GAC CCT GTA CGA CCC GCT GGT GGC AAC GCC GAT GAG TGC GCC GAC
 gly val his ser asp asp pro val arg pro ala gly gly asn ala asp glu cys ala asp
 183/61
 GAA GGC CGA GCG ACG GGC TGC CGG CGC TGA CCG CCG CGG AAG CCG CCG AGT GGA TGG TCA
 glu gly arg ala thr gly cys arg arg OPA pro pro arg lys pro pro ser gly trp ser
 243/81
 CCA CCG CCC GCA CCC GAC CGG TAC GGA TCG CGC CTC GGG TTA CCG TCG CCG TCA ACG CGC
 pro pro pro ala pro asp arg tyr gly ser arg leu gly leu pro ser pro ser thr arg
 303/101
 TGG ACA GCA TCG GTC CCC GCT GGG TCA ATG CAC TCA TGC AGC GCC GCA ACG AAC AGC TCA
 trp thr ala ser val pro ala gly ser met his ser cys ser ala ala thr asn ser ser
 363/121
 ACC CTT GAA CCG GGT CCC GGC CTG CCG ACC CTC GGC CGC CGG CGT GCC GCT ACG TGA TAG
 thr leu glu pro gly pro gly leu pro thr leu gly arg arg arg ala ala thr OPA AMB
 423/141
 ACA CAG GGC CAT GGA AAT CCT GGC CAG CCG GAT GCT ACT TCG GCC GGC GGA CTA TCA GCG
 thr gln gly his gly asn pro gly gln pro asp ala thr ser ala gly gly leu ser ala
 483/161
 GTC GCT GAG CTT CTA CCG TGA CCA GAT C
 val ala glu leu leu pro OPA pro asp

SEQ ID No.11C

FIGURE 11C

part of the nucleotide sequence of Seq11

1/1
 CGT CGC CGT CAA CGC GCT GGA CAG CAT CGG TCC CCG CTG GGT CAA TGC ACT CAT GCA GCG
 arg arg arg gln arg ala gly gln his arg ser pro leu gly gln cys thr his ala ala
 61/21
 CCG CAA CGA ACA GCT CAA CCC TTG AAC CGG GTC CCG GCC TGC CGA CCC TCG GCC GCC GGC
 pro gln arg thr ala gln pro leu asn arg val pro ala cys arg pro ser ala ala gly
 121/41
 GTG CCG CTA CGT GAT AGA CAC AGG GCC ATG GAA ATC CTG GCC AGC CGG ATG CTA CTT CGG
 val pro leu arg asp arg his arg ala met glu ile leu ala ser arg met leu leu arg
 181/61
 CCG GCG GAC TAT CAG CGG TCG CTG AGC TTC TAC CGT GAC CAG ATC
 pro ala asp tyr gln arg ser leu ser phe tyr arg asp gln ile

SEQ ID No.11A'

FIGURE 11A'

34/185

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1/1                               31/11
GTC GCC GTC AAC GCG CTG GAC AGC ATC GGT CCC CGC TGG GTC AAT GCA CTC ATG CAG CGC
val ala val asn ala leu asp ser ile gly pro arg trp val asn ala leu met gln arg
61/21                               91/31
CGC AAC GAA CAG CTC AAC CCT TGA ACC GGG TCC CGG CCT GCC GAC CCT CGG CCG CCG GCG
arg asn glu gln leu asn pro OPA thr gly ser arg pro ala asp pro arg pro pro ala
121/41                               151/51
TGC CGC TAC GTG ATA GAC ACA GGG CCA TGG AAA TCC TGG CCA GCC GGA TGC TAC TTC GGC
cys arg tyr val ile asp thr gly pro trp lys ser trp pro ala gly cys tyr phe gly
181/61                               211/71
CGG CGG ACT ATC AGC GGT CGC TGA GCT TCT ACC GTG ACC AGA TC
arg arg thr ile ser gly arg OPA ala ser thr val thr arg

```

SEQ ID No.11B'

FIGURE 11B'

```

1/1                               31/11
TCG CCG TCA ACG CGC TGG ACA GCA TCG GTC CCC GCT GGG TCA ATG CAC TCA TGC AGC GCC
ser pro ser thr arg trp thr ala ser val pro ala gly ser met his ser cys ser ala
61/21                               91/31
GCA ACG AAC AGC TCA ACC CTT GAA CCG GGT CCC GGC CTG CCG ACC CTC GGC CGC CGG CGT
ala thr asn ser ser thr leu glu pro gly pro gly leu pro thr leu gly arg arg arg
121/41                               151/51
GCC GCT ACG TGA TAG ACA CAG GGC CAT GGA AAT CCT GGC CAG CCG GAT GCT ACT TCG GCC
ala ala thr OPA AMB thr gln gly his gly asn pro gly gln pro asp ala thr ser ala
181/61                               211/71
GGC GGA CTA TCA GCG GTC GCT GAG CTT CTA CCG TGA CCA GAT C
gly gly leu ser ala val ala glu leu leu pro OPA pro asp

```

SEQ ID No.11C'

FIGURE 11C'

sequence Rv0546c predicted by Cole et al. (Nature 393:537-544) and containing Seq11A'

```

1/1                               31/11
atg gaa atc ctg gcc agc cgg atg cta ctt cgg cgg gcg gac tat cag cgg tcg ctg agc
Met glu ile leu ala ser arg met leu leu arg pro ala asp tyr gln arg ser leu ser
61/21                               91/31
ttc tac cgt gac cag atc ggg ctg gcg att gcc cgt gaa tac ggg gcc ggc aca gtg ttt
phe tyr arg asp gln ile gly leu ala ile ala arg glu tyr gly ala gly thr val phe
121/41                               151/51
ttc gcc ggt cag tca ctg ctc gaa ctg gcc ggt tac ggc gag cgg gac cat tcg cgg gga
phe ala gly gln ser leu leu glu leu ala gly tyr gly glu pro asp his ser arg gly
181/61                               211/71
cct ttt ccc ggc gcg ctg tgg ctg cag gtg cgc gac ctc gag gct acc cag acc gag ctg
pro phe pro gly ala leu trp leu gln val arg asp leu glu ala thr gln thr glu leu
241/81                               271/91
gtc agc cga ggc gtg tcg atc gct cgc gag ccc cgc cgc gaa cgg tgg ggc ctg cac gag
val ser arg gly val ser ile ala arg glu pro arg arg glu pro trp gly leu his glu
301/101                               331/111
atg cat gtg acc gac cca gac ggg atc aca ctg ata ttc gtc gag gtt ccc gag ggt cac
met his val thr asp pro asp gly ile thr leu ile phe val glu val pro glu gly his
361/121
ccg ctg cgt aca gac acc cgg gcg tga
pro leu arg thr asp thr arg ala OPA

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SEQ ID No.11D

FIGURE 11D

REPLACEMENT SHEET (RULE 26)

REPLACEMENT SHEET (RULE 26)

ORF predicted by Cole et al. (Nature 393:537-544) and containing Rv0546c

1/1	31/11
tag tca ggg cgt gca ttc gac gac gct gta	cta ccc gct ggt ggc aac tcc gat gat tgc
AMB ser gly arg ala phe asp asp ala val	leu pro ala gly gly asn ser asp asp cys
61/21	91/31
gcc gac gaa ggc cta cga cgg gct gcc ggc	gct gac cgc cgc gga agc cgc cga gtg gat
ala asp glu gly leu arg arg ala ala gly	ala asp arg arg gly ser arg arg val asp
121/41	151/51
ggt cac cgc cgc ccg cac ccg acc ggt gcg	gat cgc gcc tcg ggt tgc cgt cgc cgt caa
gly his arg arg pro his pro thr gly ala	asp arg ala ser gly cys arg arg arg gln
181/61	211/71
cgc gct gga cag cat cgg tcc ccg ctg ggt	caa tgc act cat gca gcg ccg caa cga aca
arg ala gly gln his arg ser pro leu gly	gln cys thr his ala ala pro gln arg thr
241/81	271/91
gct caa ccc ttg aac cgg gtc ccg gcc tgc	cga ccc tcg gcc gcc ggc gtg ccg cta cgt
ala gln pro leu asn arg val pro ala cys	arg pro ser ala ala gly val pro leu arg
301/101	331/111
gat aga cac agg gcc atg gaa atc ctg gcc	agc cgg atg cta ctt cgg ccg gcg gac tat
asp arg his arg ala met glu ile leu ala	ser arg met leu leu arg pro ala asp tyr
361/121	391/131
cag cgg tcg ctg agc ttc tac cgt gac cag	atc ggg ctg gcg att gcc cgt gaa tac ggg
gln arg ser leu ser phe tyr arg asp gln	ile gly leu ala ile ala arg glu tyr gly
421/141	451/151
gcc ggc aca gtg ttt ttc gcc ggt cag tca	ctg ctc gaa ctg gcc ggt tac ggc gag ccg
ala gly thr val phe phe ala gly gln ser	leu leu glu leu ala gly tyr gly glu pro
481/161	511/171
gac cat tcg cgg gga cct ttt ccc gcc gcg	ctg tgg ctg cag gtg cgc gac ctc gag gct
asp his ser arg gly pro phe pro gly ala	leu trp leu gln val arg asp leu glu ala
541/181	571/191
acc cag acc gag ctg gtc agc cga ggc gtg	tcg atc gct cgc gag ccc cgc cgc gaa ccg
thr gln thr glu leu val ser arg gly val	ser ile ala arg glu pro arg arg glu pro
601/201	631/211
tgg ggc ctg cac gag atg cat gtg acc gac	cca gac ggg atc aca ctg ata ttc gtc gag
trp gly leu his glu met his val thr asp	pro asp gly ile thr leu ile phe val glu
661/221	691/231
gtt ccc gag ggt cac ccg ctg cgt aca gac	acc cgg gcg tga
val pro glu gly his pro leu arg thr asp	thr arg ala OPA

SEQ ID No.11F

FIGURE 11F

1/1 31/11
gac cga agg gat ttc gcg act aac tcg gcc tgt aag gca acg cga ggt ctt cat gcc gag
asp arg arg asp phe ala thr asn ser ala cys lys ala thr arg gly leu his ala glu
61/21 91/31
gac gta gac agg aag aga cag gga agc tga tga cgt cgc gta ccg gac cgc cat tct gtc
asp val asp arg lys arg gln gly ser OPA OPA arg arg val pro asp arg his ser val
121/41 151/51
gag tct ttc cga gtt cag caa caa tcg aca cag aag cgg gga cca gac cgg gag gac gac
glu ser phe arg val gln gln gln ser thr gln lys arg gly pro asp arg glu asp asp
181/61 211/71
gcg gcc cgg gcc gct tcg ggc cga gtg tct gag taa gac cag agt cac ggg tcc gtg tgt
ala ala arg ala ala ser gly arg val ser glu OCH asp gln ser his gly ser val cys
241/81 271/91
gac aac cgc gcg gaa ttc aat cgg atg gcg ggc ggg acc gga ttg cgc cgg tca ccg agg
asp asn arg ala glu phe asn arg met ala gly gly thr gly leu arg arg ser pro arg
301/101
aac ctc cgg agt gat c
asn leu arg ser asp

SEQ ID No.12A

FIGURE 12A

1/1 31/11
acc gaa ggg att tcg cga cta act cgg cct gta agg caa cgc gag gtc ttc atg ccg agg
thr glu gly ile ser arg leu thr arg pro val arg gln arg glu val phe met pro arg
61/21 91/31
acg tag aca gga aga gac agg gaa gct gat gac gtc gcg tac cgg acc gcc att ctg tcg
thr AMB thr gly arg asp arg glu ala asp asp val ala tyr arg thr ala ile leu ser
121/41 151/51
agt ctt tcc gag ttc agc aac aat cga cac aga agc ggg gac cag acc ggg agg acg acg
ser leu ser glu phe ser asn asn arg his arg ser gly asp gln thr gly arg thr thr
181/61 211/71
cgg ccc ggg ccg ctt cgg gcc gag tgt ctg agt aag acc aga gtc acg ggt ccg tgt gtg
arg pro gly pro leu arg ala glu cys leu ser lys thr arg val thr gly pro cys val
241/81 271/91
aca acc gcg cgg aat tca atc gga tgg cgg gcg gga ccg gat tgc gcc ggt cac cga gga
thr thr ala arg asn ser ile gly trp arg ala gly pro asp cys ala gly his arg gly
301/101
acc tcc gga gtg atc
thr ser gly val ile

SEQ ID No.12B

FIGURE 12B

37/185

1/1	31/11
ccg aag gga ttt cgc gac taa ctc ggc ctg	taa ggc aac gcg agg tct tca tgc cga gga
pro lys gly phe arg asp OCH leu gly leu	UCH gly asn ala arg ser ser cys arg gly
61/21	91/31
cgt aga cag gaa gag aca ggg aag ctg atg	acg tcg cgt acc gga ccg cca ttc tgt cga
arg arg gln glu glu thr gly lys leu met	thr ser arg thr gly pro pro phe cys arg
121/41	151/51
gtc ttt ccg agt tca gca aca atc gac aca	gaa gcg ggg acc aga ccg gga gga cga cgc
val phe pro ser ser ala thr ile asp thr	glu ala gly thr arg pro gly gly arg arg
181/61	211/71
ggc ccg ggc cgc ttc ggg ccg agt gtc tga	gta aga cca gag tca cgg gtc cgt gtg tga
gly pro gly arg phe gly pro ser val OPA	val arg pro glu ser arg val arg val OPA
241/81	271/91
caa ccg cgc gga att caa tcg gat ggc ggg	cgg gac cgg att gcg ccg gtc acc gag gaa
gln pro arg gly ile gln ser asp gly gly	arg asp arg ile ala pro val thr glu glu
301/101	
cct ccg gag tga tc	
pro pro glu OPA	

SEQ ID No.12C

FIGURE 12C

1/1	31/11
GGG ATT TCG TTG CCC GAT GGA TTG TTT GTA	CGG TTT GGG AAA AAC ACT TGA AGT CCT TTT
gly ile ser leu pro asp gly leu phe val	arg phe gly lys asn thr OPA ser pro phe
61/21	91/31
TAT TGG CAA TGC TGG AAA TGG ACA TTC CAA	TAT TGC GCG AAT TAA CCG AAC ACG GTG AGG
tyr trp gln cys trp lys trp thr phe gln	tyr cys ala asn OCH pro asn thr val arg
121/41	151/51
GGG GGG CAA GCG TTT GTA CCG GGG CCA GCA	AGC GCC GCC GAC CGG TTG ACC GAA GCC AGC
gly gly gln ala phe val pro gly pro ala	ser ala ala asp arg leu thr glu ala ser
181/61	211/71
ATG TTG TTG TGT CAG CGC GGG CTT GGT CTC	GAT GTC CCG GCC TTG GCT GGA CCC GCT TCT
met leu leu cys gln arg gly leu gly leu	asp val pro ala leu ala gly pro ala ser
241/81	271/91
TCA AAA CAG GTT GAA CTT AAC GAC TCA AGA	ACG GAA ACG CTT GAA CCG CGA CGT CGC TCC
ser lys gln val glu leu asn asp ser arg	thr glu thr leu glu pro arg arg arg ser
301/101	331/111
GGA CAC CAA TTT GAC TCG GCT CTT TGG CAA	TTG AAG GTG AGC TGC GAG CAG CCG GGT GAC
gly his gln phe asp ser ala leu trp gln	leu lys val ser cys glu gln pro gly asp
361/121	391/131
CGC ATC GTT GGC CTT GCC ATC AAT CGC CGG	CTC GCG GAC GTA GAT AAT CAG CTC ACC GTT
arg ile val gly leu ala ile asn arg arg	leu ala asp val asp asn gln leu thr val
421/141	451/151
GGG ACC GAC CTC GAC CAG GGG TCC TTT GTG	ACT GCC GGG CTT GAC GCG GAC GAC CAC AGA
gly thr asp leu asp gln gly ser phe val	thr ala gly leu asp ala asp asp his arg
481/161	511/171
GTC GGT CAT CGC CTA AGG CTA CCG TTC TGA	CCT GGG GCT GCG TGG GCG CCG ACG ACG TGA
val gly his arg leu arg leu pro phe OPA	pro gly ala ala trp ala pro thr thr OPA
541/181	571/191
GGC ACG TCA TGT CTC AGC GGC CCA CCG CCA	CCT CGG TCG CCG GCA GTA TGT CAG CAT GTG
gly thr ser cys leu ser gly pro pro pro	pro arg ser pro ala val cys gln his val
601/201	631/211
CAG ATG ACT CCA CGC AGC CTT GTT CGC ATC	GTT GGT GTC GTG GTT GCG ACG ACC TTG GCG
gln met thr pro arg ser leu val arg ile	val gly val val val ala thr thr leu ala
661/221	691/231
CTG GTG AGC GCA CCC GCC GGC GGT CGT GCC	GCG CAT GCG GAT C
leu val ser ala pro ala gly gly arg ala	ala his ala asp

SEQ ID No.13A

FIGURE 13A

32/11
 GGA TTT CGT TGC CCG ATG GAT TGT TTG TAC GGT TTG GGA AAA ACA CTT GAA GTC CTT TTT
 gly phe arg cys pro met asp cys leu tyr gly leu gly lys thr leu glu val leu phe
 62/21 92/31
 ATT GGC AAT GCT GGA AAT GGA CAT TCC AAT ATT GCG CGA ATT AAC CGA ACA CGG TGA GGG
 ile gly asn ala gly asn gly his ser asn ile ala arg ile asn arg thr arg OPA gly
 122/41 152/51
 GGG GGC AAG CGT TTG TAC CGG GGC CAG CAA GCG CCG CCG ACC GGT TGA CCG AAG CCA GCA
 gly gly lys arg leu tyr arg gly gln gln ala pro pro thr gly OPA pro lys pro ala
 182/61 212/71
 TGT TGT TGT GTC AGC GCG GGC TTG GTC TCG ATG TCC CGG CCT TGG CTG GAC CCG CTT CTT
 cys cys cys val ser ala gly leu val ser met ser arg pro trp leu asp pro leu leu
 242/81 272/91
 CAA AAC AGG TTG AAC TTA ACG ACT CAA GAA CGG AAA CGC TTG AAC CGC GAC GTC GCT CCG
 gln asn arg leu asn leu thr thr gln glu arg lys arg leu asn arg asp val ala pro
 302/101 332/111
 GAC ACC AAT TTG ACT CGG CTC TTT GGC AAT TGA AGG TGA GCT GCG AGC AGC CGG GTG ACC
 asp thr asn leu thr arg leu phe gly asn OPA arg OPA ala ala ser ser arg val thr
 362/121 392/131
 GCA TCG TTG GCC TTG CCA TCA ATC GCC GGC TCG CGG ACG TAG ATA ATC AGC TCA CCG TTG
 ala ser leu ala leu pro ser ile ala gly ser arg thr AMB ile ile ser ser pro leu
 422/141 452/151
 GGA CCG ACC TCG ACC AGG GGT CCT TTG TGA CTG CCG GGC TTG ACG CGG ACG ACC ACA GAG
 gly pro thr ser thr arg gly pro leu OPA leu pro gly leu thr arg thr thr thr glu
 482/161 512/171
 TCG GTC ATC GCC TAA GGC TAC CGT TCT GAC CTG GGG CTG CGT GGG CGC CGA CGA CGT GAG
 ser val ile ala OCH gly tyr arg ser asp leu gly leu arg gly arg arg arg arg glu
 542/181 572/191
 GCA CGT CAT GTC TCA GCG GCC CAC CGC CAC CTC GGT CGC CGG CAG TAT GTC AGC ATG TGC
 ala arg his val ser ala ala his arg his leu gly arg arg gln tyr val ser met cys
 602/201 632/211
 AGA TGA CTC CAC GCA GCC TTG TTC GCA TCG TTG GTG TCG TGG TTG CGA CGA CCT TGG CGC
 arg OPA leu his ala ala leu phe ala ser leu val ser trp leu arg arg pro trp arg
 662/221 692/231
 TGG TGA GCG CAC CCG CCG GCG GTC GTG CCG CGC ATG CGG ATC
 trp OPA ala his pro pro ala val val pro arg met arg ile

SEQ ID No.13B

FIGURE 13B

33/11
 GAT TTC GTT GCC CGA TGG ATT GTT TGT ACG GTT TGG GAA AAA CAC TTG AAG TCC TTT TTA
 asp phe val ala arg trp ile val cys thr val trp glu lys his leu lys ser phe leu
 63/21
 93/31
 TTG GCA ATG CTG GAA ATG GAC ATT CCA ATA TTG CGC GAA TTA ACC GAA CAC GGT GAG GGG
 leu ala met leu glu met asp ile pro ile leu arg glu leu thr glu his gly glu gly
 123/41
 153/51
 GGG GCA AGC GTT TGT ACC GGG GCC AGC AAG CGC CGC CGA CCG GTT GAC CGA AGC CAG CAT
 gly ala ser val cys thr gly ala ser lys arg arg arg pro val asp arg ser gln his
 183/61
 213/71
 GTT GTT GTG TCA GCG CGG GCT TGG TCT CGA TGT CCC GGC CTT GGC TGG ACC CGC TTC TTC
 val val val ser ala arg ala trp ser arg cys pro gly leu gly trp thr arg phe phe
 243/81
 273/91
 AAA ACA GGT TGA ACT TAA CGA CTC AAG AAC GGA AAC GCT TGA ACC GCG ACG TCG CTC CGG
 lys thr gly OPA thr OCH arg leu lys asn gly asn ala OPA thr ala thr ser leu arg
 303/101
 333/111
 ACA CCA ATT TGA CTC GGC TCT TTG GCA ATT GAA GGT GAG CTG CGA GCA GCC GGG TGA CCG
 thr pro ile OPA leu gly ser leu ala ile glu gly glu leu arg ala ala gly OPA pro
 363/121
 393/131
 CAT CGT TGG CCT TGC CAT CAA TCG CCG GCT CGC GGA CGT AGA TAA TCA GCT CAC CGT TGG
 his arg trp pro cys his gln ser pro ala arg gly arg arg OCH ser ala his arg trp
 423/141
 453/151
 GAC CGA CCT CGA CCA GGG GTC CTT TGT GAC TGC CGG GCT TGA CGC GGA CGA CCA CAG AGT
 asp arg pro arg pro gly val leu cys asp cys arg ala OPA arg gly arg pro gln ser
 483/161
 513/171
 CGG TCA TCG CCT AAG GCT ACC GTT CTG ACC TGG GGC TGC GTG GGC GCC GAC GAC GTG AGG
 arg ser ser pro lys ala thr val leu thr trp gly cys val gly ala asp asp val arg
 543/181
 573/191
 CAC GTC ATG TCT CAG CGG CCC ACC GCC ACC TCG GTC GCC GGC AGT ATG TCA GCA TGT GCA
 his val met ser gln arg pro thr ala thr ser val ala gly ser met ser ala cys ala
 603/201
 633/211
 GAT GAC TCC ACG CAG CCT TGT TCG CAT CGT TGG TGT CGT GGT TGC GAC GAC CTT GGC GCT
 asp asp ser thr gln pro cys ser his arg trp cys arg gly cys asp asp leu gly ala
 663/221
 693/231
 GGT GAG CGC ACC CGC CGG CGG TCG TGC CGC GCA TGC GGA TC
 gly glu arg thr arg arg arg ser cys arg ala cys gly

SEQ ID No.13C

FIGURE 13C

part of the nucleotide sequence of seq13A

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1/1                               31/11
GGG TCC TTT GTG ACT GCC GGG CTT GAC GCG GAC GAC CAC AGA GTC GGT CAT CGC CTA AGG
gly ser phe val thr ala gly leu asp ala asp asp his arg val gly his arg leu arg
61/21                               91/31
CTA CCG TTC TGA CCT GGG GCT GCG TGG GCG CCG ACG ACG TGA GGC ACG TCA TGT CTC AGC
leu pro phe OPA pro gly ala ala trp ala pro thr thr OPA gly thr ser cys leu ser
121/41                               151/51
GGC CCA CCG CCA CCT CGG TCG CCG GCA GTA TGT CAG CAT GTG CAG ATG ACT CCA CGC AGC
gly pro pro pro pro arg ser pro ala val cys gln his val gln met thr pro arg ser
181/61                               211/71
CTT GTT CGC ATC GTT GGT GTC GTG GTT GCG ACG ACC TTG GCG CTG GTG AGC GCA CCC GCC
leu val arg ile val gly val val val ala thr thr leu ala leu val ser ala pro ala
241/81
GGC GGT CGT GCC GCG CAT GCG GAT C
gly gly arg ala ala his ala asp

```

SEQ ID No.13A'

FIGURE 13A'

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1/1                               31/11
GGT CCT TTG TGA CTG CCG GGC TTG ACG CGG ACG ACC ACA GAG TCG GTC ATC GCC TAA GGC
gly pro leu OPA leu pro gly leu thr arg thr thr thr glu ser val ile ala OCH gly
61/21                               91/31
TAC CGT TCT GAC CTG GGG CTG CGT GGG CGC CGA CGA CGT GAG GCA CGT CAT GTC TCA GCG
tyr arg ser asp leu gly leu arg gly arg arg arg glu ala arg his val ser ala
121/41                               151/51
GCC CAC CGC CAC CTC GGT CGC CGG CAG TAT GTC AGC ATG TGC AGA TGA CTC CAC GCA GCC
ala his arg his leu gly arg arg gln tyr val ser met cys arg OPA leu his ala ala
181/61                               211/71
TTG TTC GCA TCG TTG GTG TCG TGG TTG CGA CGA CCT TGG CGC TGG TGA GCG CAC CCG CCG
leu phe ala ser leu val ser trp leu arg arg pro trp arg trp OPA ala his pro pro
241/81
GCG GTC GTG CCG CGC ATG CGG ATC
ala val val pro arg met arg ile

```

SEQ ID No.13B'

FIGURE 13B'

```

1/1                               31/11
GTC CTT TGT GAC TGC CGG GCT TGA CGC GGA CGA CCA CAG AGT CGG TCA TCG CCT AAG GCT
val leu cys asp cys arg ala OPA arg gly arg pro gln ser arg ser ser pro lys ala
61/21                               91/31
ACC GTT CTG ACC TGG GGC TGC GTG GGC GCC GAC GAC GTG AGG CAC GTC ATG TCT CAG CGG
thr val leu thr trp gly cys val gly ala asp asp val arg his val met ser gln arg
121/41                               151/51
CCC ACC GCC ACC TCG GTC GCC GGC AGT ATG TCA GCA TGT GCA GAT GAC TCC ACG CAG CCT
pro thr ala thr ser val ala gly ser met ser ala cys ala asp asp ser thr gln pro
181/61                               211/71
TGT TCG CAT CGT TGG TGT CGT GGT TGC GAC GAC CTT GGC GCT GGT GAG CGC ACC CGC CGG
cys ser his arg trp cys arg gly cys asp asp leu gly ala gly glu arg thr arg arg
241/81
CGG TCG TGC CGC GCA TGC GGA TC
arg ser cys arg ala cys gly

```

SEQ ID No.13C'

FIGURE 13C'

sequence Rv1984c predicted by Cole et al. (Nature 393:537-544) and containing seq13A'

1/1	31/11
atg act cca cgc agc ctt gtt cgc atc gtt	ggt gtc gtg gtt gcg acg acc ttg gcg ctg
Met thr pro arg ser leu val arg ile val	gly val val val ala thr thr leu ala leu
61/21	91/31
gtg agc gca ccc gcc gcc ggt cgt gcc gcg	cat gcg gat ccg tgt tcg gac atc gcg gtc
val ser ala pro ala gly gly arg ala ala	his ala asp pro cys ser asp ile ala val
121/41	151/51
ggt ttc gct cgc gcc acg cat cag gct tct	ggt ctt gcc gac gtc ggt gag gcg ttc gtc
val phe ala arg gly thr his gln ala ser	gly leu gly asp val gly glu ala phe val
181/61	211/71
gac tcg ctt acc tcg caa gtt gcc gcc cgg	tcg att ggg gtc tac gcg gtg aac tac cca
asp ser leu thr ser gln val gly gly arg	ser ile gly val tyr ala val asn tyr pro
241/81	271/91
gca agc gac gac tac cgc gcg agc gcg tca	aac ggt tcc gat gat gcg agc gcc cac atc
ala ser asp asp tyr arg ala ser ala ser	asn gly ser asp asp ala ser ala his ile
301/101	331/111
cag cgc acc gtc gcc agc tgc ccg aac acc	agg att gtg ctt ggt gcc tat tcg cag ggt
gln arg thr val ala ser cys pro asn thr	arg ile val leu gly gly tyr ser gln gly
361/121	391/131
gcg acg gtc atc gat ttg tcc acc tcg gcg	atg ccg ccc gcg gtg gca gat cat gtc gcc
ala thr val ile asp leu ser thr ser ala	met pro pro ala val ala asp his val ala
421/141	451/151
gct gtc gcc ctt ttc gcc gag cca tcc agt	ggt ttc tcc agc atg ttg tgg gcc gcc ggg
ala val ala leu phe gly glu pro ser ser	gly phe ser ser met leu trp gly gly gly
481/161	511/171
tcg ttg ccg aca atc ggt ccg ctg tat agc	tct aag acc ata aac ttg tgt gct ccc gac
ser leu pro thr ile gly pro leu tyr ser	ser lys thr ile asn leu cys ala pro asp
541/181	571/191
gat cca ata tgc acc gga gcc gcc aat att	atg gcg cat gtt tcg tat gtt cag tcg ggg
asp pro ile cys thr gly gly gly asn ile	met ala his val ser tyr val gln ser gly
601/201	631/211
atg aca agc cag gcg gcg aca ttc gcg gcg	aac agg ctc gat cac gcc gga tga
met thr ser gln ala ala thr phe ala ala	asn arg leu asp his ala gly OPA

SEQ ID No.13D

FIGURE 13D

Seq13F: ORF predicted by Cole et al. (Nature 393:537-544) and containing Rv1984c

1/1	31/11
tga ggc acg tca tgt ctc agc ggc cca ccg	cca cct cgg tcg ccg gca gta tgt cag cat
OPA gly thr ser cys leu ser gly pro pro	pro pro arg ser pro ala val cys gln his
61/21	91/31
gtg cag atg act cca cgc agc ctt gtt cgc	atc gtt ggt gtc gtg gtt gcg acg acc ttg
val gln met thr pro arg ser leu val arg	ile val gly val val val ala thr thr leu
121/41	151/51
gcg ctg gtg agc gca ccc gcc ggc ggt cgt	gcc gcg cat gcg gat ccg tgt tcg gac atc
ala leu val ser ala pro ala gly gly arg	ala ala his ala asp pro cys ser asp ile
181/61	211/71
gcg gtc gtt ttc gct cgc ggc acg cat cag	gct tct ggt ctt ggc gac gtc ggt gag gcg
ala val val phe ala arg gly thr his gln	ala ser gly leu gly asp val gly glu ala
241/81	271/91
ttc gtc gac tcg ctt acc tcg caa gtt ggc	ggg cgg tcg att ggg gtc tac gcg gtg aac
phe val asp ser leu thr ser gln val gly	gly arg ser ile gly val tyr ala val asn
301/101	331/111
tac cca gca agc gac gac tac cgc gcg agc	gcg tca aac ggt tcc gat gat gcg agc gcc
tyr pro ala ser asp asp tyr arg ala ser	ala ser asn gly ser asp asp ala ser ala
361/121	391/131
cac atc cag cgc acc gtc gcc agc tgc ccg	aac acc agg att gtg ctt ggt ggc tat tcg
his ile gln arg thr val ala ser cys pro	asn thr arg ile val leu gly gly tyr ser
421/141	451/151
cag ggt gcg acg gtc atc gat ttg tcc acc	tcg gcg atg ccg ccc gcg gtg gca gat cat
gln gly ala thr val ile asp leu ser thr	ser ala met pro pro ala val ala asp his
481/161	511/171
gtc gcc gct gtc gcc ctt ttc ggc gag cca	tcc agt ggt ttc tcc agc atg ttg tgg ggc
val ala ala val ala leu phe gly glu pro	ser ser gly phe ser ser met leu trp gly
541/181	571/191
ggc ggg tcg ttg ccg aca atc ggt ccg ctg	tat agc tct aag acc ata aac ttg tgt gct
gly gly ser leu pro thr ile gly pro leu	tyr ser ser lys thr ile asn leu cys ala
601/201	631/211
ccc gac gat cca ata tgc acc gga ggc ggc	aat att atg gcg cat gtt tcg tat gtt cag
pro asp asp pro ile cys thr gly gly gly	asn ile met ala his val ser tyr val gln
661/221	691/231
tcg ggg atg aca agc cag gcg gcg aca ttc	gcg gcg aac agg ctc gat cac gcc gga tga
ser gly met thr ser gln ala ala thr phe	ala ala asn arg leu asp his ala gly OPA

SEQ ID No.13F

FIGURE 13F

31/11
 CCA CCG GGG CTG GAG GGG CGA ATG TGC GCC GAA CGC CGT CGG CCA ACT TGG CCG CTG AGG
 pro pro gly leu glu gly arg met cys ala glu arg arg arg pro thr trp pro leu arg
 61/21 91/31
 GCG GCT GAT CCC CTG GCC CGA GAC GGG GCA AGC CAA TAG CGG CTC CAT CGG GCT TTG CTG
 ala ala asp pro leu ala arg asp gly ala ser gln AMB arg leu his arg ala leu leu
 121/41 151/51
 GTA GCG GTT CGG CGG GAA CCG AGC GCC GAC GTT GTC GGT GCC CGG TGA TAT ATT GGG TCA
 val ala val arg arg glu pro ser ala asp val val gly ala arg OPA tyr ile gly ser
 181/61 211/71
 GAC GGG TAT GGC GGC GAC TGA GGT GAT CTG CGA CAC GCC GCC GCG GTG CTC GAG CCA GGC
 asp gly tyr gly gly asp OPA gly asp leu arg his ala ala ala val leu glu pro gly
 241/81 271/91
 TTA CGA CCA GGG AAT TTC GAA AAT GTT ATT CAG AAC ATC TTG TAT CTC TTC CTC CGT GCC
 leu arg pro gly asn phe glu asn val ile gln asn ile leu tyr leu phe leu arg ala
 301/101 331/111
 ACC CCC TAG GTG TAG TGT TTT CGA GTA CCG GCA GAT CCC AGT TCA CCA GTC TCA CCA GAT
 thr pro AMB val AMB cys phe arg val pro ala asp pro ser ser pro val ser pro asp

C

SEQ ID No.14A

FIGURE 14A

32/11
 CAC CGG GGC TGG AGG GGC GAA TGT GCG CCG AAC GCC GTC GGC CAA CTT GGC CGC TGA GGG
 his arg gly trp arg gly glu cys ala pro asn ala val gly gln leu gly arg OPA gly
 62/21 92/31
 CGG CTG ATC CCC TGG CCC GAG ACG GGG CAA GCC AAT AGC GGC TCC ATC GGG CTT TGC TGG
 arg leu ile pro trp pro glu thr gly gln ala asn ser gly ser ile gly leu cys trp
 122/41 152/51
 TAG CGG TTC GGC GGC AAC CGA GCG CCG ACG TTG TCG GTG CCC GGT GAT ATA TTG GGT CAG
 AMB arg phe gly gly asn arg ala pro thr leu ser val pro gly asp ile leu gly gln
 182/61 212/71
 ACG GGT ATG GCG GCG ACT GAG GTG ATC TGC GAC ACG CCG CCG CGG TGC TCG AGC CAG GCT
 thr gly met ala ala thr glu val ile cys asp thr pro pro arg cys ser ser gln ala
 242/81 272/91
 TAC GAC CAG GGA ATT TCG AAA ATG TTA TTC AGA ACA TCT TGT ATC TCT TCC TCC GTG CCA
 tyr asp gln gly ile ser lys met leu phe arg thr ser cys ile ser ser ser val pro
 302/101 332/111
 CCC CCT AGG TGT AGT GTT TTC GAG TAC CGG CAG ATC CCA GTT CAC CAG TCT CAC CAG ATC
 pro pro arg cys ser val phe glu tyr arg gln ile pro val his gln ser his gln ile

SEQ ID No.14B

FIGURE 14B

44/185

33/11
ACC GGG GCT GGA GGG GCG AAT GTG CGC CGA ACG CCG TCG GCC AAC TTG GCC GCT GAG GGC
thr gly ala gly gly ala asn val arg arg thr pro ser ala asn leu ala ala glu gly
63/21 93/31
GGC TGA TCC CCT GGC CCG AGA CGG GGC AAG CCA ATA GCG GCT CCA TCG GGC TTT GCT GGT
gly OPA ser pro gly pro arg arg gly lys pro ile ala ala pro ser gly phe ala gly
123/41 153/51
AGC GGT TCG GCG GGA ACC GAG CGC CGA CGT TGT CGG TGC CCG GTG ATA TAT TGG GTC AGA
ser gly ser ala gly thr glu arg arg arg cys arg cys pro val ile tyr trp val arg
183/61 213/71
CGG GTA TGG CGG CGA CTG AGG TGA TCT GCG ACA CGC CGC CGC GGT GCT CGA GCC AGG CTT
arg val trp arg arg leu arg OPA ser ala thr arg arg arg gly ala arg ala arg leu
243/81 273/91
ACG ACC AGG GAA TTT CGA AAA TGT TAT TCA GAA CAT CTT GTA TCT CTT CCT CCG TGC CAC
thr thr arg glu phe arg lys cys tyr ser glu his leu val ser leu pro pro cys his
303/101 333/111
CCC CTA GGT GTA GTG TTT TCG AGT ACC GGC AGA TCC CAG TTC ACC AGT CTC ACC AGA TC
pro leu gly val val phe ser ser thr gly arg ser gln phe thr ser leu thr arg

SEQ ID No.14C

FIGURE 14C

part of the nucleotide sequence of seq14A

1/1 31/11
TTT TCG AGT ACC GGC AGA TCC CAG GTT CAC CAG GTC TCA CCA GAT C
phe ser ser thr gly arg ser gln val his gln val ser pro asp

SEQ ID No.14A'

FIGURE 14A'

1/1 31/11
TGT TTT CGA GTA CCG GCA GAT CCC AGG TTC ACC AGG TCT CAC CAG ATC
cys phe arg val pro ala asp pro arg phe thr arg ser his gln ile

SEQ ID No.14C

FIGURE 14C

1/1 31/11
GTT TTC GAG TAC CGG CAG ATC CCA GGT TCA CCA GGT CTC ACC AGA TC
val phe glu tyr arg gln ile pro gly ser pro gly leu thr arg

SEQ ID No.14C'

FIGURE 14C'

ORF predicted based on the sequence published by Cole et al. (Nature 393:537-544) and containing seq14A'

1/1	31/11
TAG CGG TTC GGC GGG AAG CTA GCG GCG ACG	TTG TCG GTG GCC GGT GAT ATA TTG GGT CAG
AMB arg phe gly gly lys leu ala ala thr	leu ser val ala gly asp ile leu gly gln
61/21	91/31
ACG GGT ATG GCG GCG GCT GAG GTG ATC TGC	GAC ACG CCG CCG CGG TGC TCG AGC CAG GCT
thr gly met ala ala ala glu val ile cys	asp thr pro pro arg cys ser ser gln ala
121/41	151/51
TAC GAC CAG GGA ATT TCG AAA ATG TTA TTC	AGA ACA TCT TGT ATC TCT TCT CCG TGC CAC
tyr asp gln gly ile ser lys met leu phe	arg thr ser cys ile ser ser pro cys his
181/61	211/71
CCC CTA GGT GTA GTG TTT TCG AGT ACC GGC	AGA TCC CAG GTT CAC CAG GTC TCA CCA gat
pro leu gly val val phe ser ser thr gly	arg ser gln val his gln val ser pro asp
241/81	271/91
cca cgg ggc gcg atg aac ttc ccg gca tcg	gca tcg cca ggt cga cgg acg tgg tcg cgc
pro arg gly ala met asn phe pro ala ser	ala ser pro gly arg arg thr trp ser arg
301/101	331/111
tat gac ggg aat ctg gag cct tgt cgg gcc	gct caa cat atc gaa gat gca cta ctt gag
tyr asp gly asn leu glu pro cys arg ala	ala gln his ile glu asp ala leu leu glu
361/121	391/131
tcg ttg cca gat cct gtc aga ttc ccg att	tcc gca aag gag cgg tac gcc cat gac cgt
ser leu pro asp pro val arg phe pro ile	ser ala lys glu arg tyr ala his asp arg
421/141	
gac cgt tta cac taa	
asp arg leu his OCH	

SEQ ID No.14F

FIGURE 14F

Sequence Rv3054c predicted by Cole et al. (Nature 393:537-544)
which may be in phase with Seq14A'

1/1	31/11
gtg tca gat acc aag tcc gac atc aaa atc	ttg gcc tta gtg gga agc ctg cgc gcg gcg
val ser asp thr lys ser asp ile lys ile	leu ala leu val gly ser leu arg ala ala
61/21	91/31
tcg ttc aac cgc cag atc gcc gag ctg gct	gcc aag gtc gct ccg gac ggc gtc acc gtc
ser phe asn arg gln ile ala glu leu ala	ala lys val ala pro asp gly val thr val
121/41	151/51
acc atg ttc gag ggg ctg ggg gac ctg ccg	ttc tac aac gaa gac atc gac aca gcg acg
thr met phe glu gly leu gly asp leu pro	phe tyr asn glu asp ile asp thr ala thr
181/61	211/71
gag gtg ccg gcg ccg gtg agc gcg ttg cgg	gag gcc gcg tct gac gcg cac gct gcc ttg
glu val pro ala pro val ser ala leu arg	glu ala ala ser asp ala his ala ala leu
241/81	271/91
gtg gtc acg ccg gaa tac aac ggc agc att	ccg gcc gtg atc aag aac gcg atc gac tgg
val val thr pro glu tyr asn gly ser ile	pro ala val ile lys asn ala ile asp trp
301/101	331/111
ctg tcc agg cca ttc ggc gat ggc gcg ttg	aag gac aag ccg ttg gcc gtg atc ggc ggc
leu ser arg pro phe gly asp gly ala leu	lys asp lys pro leu ala val ile gly gly
361/121	391/131
tcc atg ggc cgc tac ggc ggg gta tgg gcg	cac gac gag act cgc aag tcg ttc agc atc
ser met gly arg tyr gly gly val trp ala	his asp glu thr arg lys ser phe ser ile
421/141	451/151
gct ggc acg cgg gtg gtc gat gcg atc aaa	ctg tcg gtg ccg ttc caa act ctg ggc aag
ala gly thr arg val val asp ala ile lys	leu ser val pro phe gln thr leu gly lys
481/161	511/171
tcg gtc gcg gac gac gcc ggg ctg gcg gcg	aat gtg cgc gac gcc gtc ggc aac ttg gcc
ser val ala asp asp ala gly leu ala ala	asn val arg asp ala val gly asn leu ala
541/181	
gct gag gtc ggc tga	
ala glu val gly OPA	

SEQ ID No.14R

FIGURE 14R

ORF predicted by Cole et al. (Nature 393:537-544) and containing Rv3054c

1/1	31/11
taa cgc gat cgg aat aaa tcg gac cat ggt	ccg gtt ggc tcg tgc aag gac gtg gac caa
OCH arg asp arg asn lys ser asp his gly	pro val gly ser cys lys asp val asp gln
61/21	91/31
caa gcg gaa agg aac gta gca gtg tca gat	acc aag tcc gac atc aaa atc ttg gcc tta
gln ala glu arg asn val ala val ser asp	thr lys ser asp ile lys ile leu ala leu
121/41	151/51
gtg gga agc ctg cgc gcg gcg tcg ttc aac	cgc cag atc gcc gag ctg gct gcc aag gtc
val gly ser leu arg ala ala ser phe asn	arg gln ile ala glu leu ala ala lys val
181/61	211/71
gct ccg gac ggc gtc acc gtc acc atg ttc	gag ggg ctg ggg gac ctg ccg ttc tac aac
ala pro asp gly val thr val thr met phe	glu gly leu gly asp leu pro phe tyr asn
241/81	271/91
gaa gac atc gac aca gcg acg gag gtg ccg	gcg ccg gtg agc gcg ttg cgg gag gcc gcg
glu asp ile asp thr ala thr glu val pro	ala pro val ser ala leu arg glu ala ala
301/101	331/111
tct gac gcg cac gct gcc ttg gtg gtc acg	ccg gaa tac aac ggc agc att ccg gcc gtg
ser asp ala his ala ala leu val val thr	pro glu tyr asn gly ser ile pro ala val
361/121	391/131
atc aag aac gcg atc gac tgg ctg tcc agg	cca ttc ggc gat ggc gcg ttg aag gac aag
ile lys asn ala ile asp trp leu ser arg	pro phe gly asp gly ala leu lys asp lys
421/141	451/151
ccg ttg gcc gtg atc ggc ggc tcc atg ggc	cgc tac ggc ggg gta tgg gcg cac gac gag
pro leu ala val ile gly gly ser met gly	arg tyr gly gly val trp ala his asp glu
481/161	511/171
act cgc aag tcg ttc agc atc gct ggc acg	cgg gtg gtc gat gcg atc aaa ctg tcg gtg
thr arg lys ser phe ser ile ala gly thr	arg val val asp ala ile lys leu ser val
541/181	571/191
ccg ttc caa act ctg ggc aag tcg gtc gcg	gac gac gcc ggg ctg gcg gcg aat gtg cgc
pro phe gln thr leu gly lys ser val ala	asp asp ala gly leu ala ala asn val arg
601/201	631/211
gac gcc gtc ggc aac ttg gcc gct gag gtc	ggc tga
asp ala val gly asn leu ala ala glu val	gly OPA

SEQ ID No.14P

FIGURE 14P

fragment based on the sequence published by Cole et al. (Nature 393:537-544) and containing seq 14F' and seq 14P'

```

1/1                                31/11
taa cgc gat cgg aat aaa tcg gac cat ggt ccg gtt ggc tcg tgc aag gac gtg gac caa
OCH arg asp arg asn lys ser asp his gly pro val gly ser cys lys asp val asp gln
asn ala ile gly ile asn arg thr met val arg leu ala arg ala arg thr trp thr asn
thr arg ser glu OCH ile gly pro trp ser gly trp leu val gln gly arg gly pro thr
61/21                                91/31
caa gcg gaa agg aac gta gca gtg tca gat acc aag tcc gac atc aaa atc ttg gcc tta
gln ala glu arg asn val ala val ser asp thr lys ser asp ile lys ile leu ala leu
lys arg lys gly thr AMB gln cys gln ile pro ser pro thr ser lys ser trp pro AMB
ser gly lys glu arg ser ser val arg tyr gln val arg his gln asn leu gly leu ser
121/41                                151/51
gtg gga agc ctg cgc gcg gcg tcg ttc aac cgc cag atc gcc gag ctg gct gcc aag gtc
val gly ser leu arg ala ala ser phe asn arg gln ile ala glu leu ala ala lys val
trp glu ala cys ala arg arg arg ser thr ala arg ser pro ser trp leu pro arg ser
gly lys pro ala arg gly val val gln pro pro asp arg arg ala gly cys gln gly arg
181/61                                211/71
gct ccg gac ggc gtc acc gtc acc atg ttc gag ggg ctg ggg gac ctg ccg ttc tac aac
ala pro asp gly val thr val thr met phe glu gly leu gly asp leu pro phe tyr asn
leu arg thr ala ser pro ser pro cys ser arg gly trp gly thr cys arg ser thr thr
ser gly arg arg his arg his his val arg gly ala gly gly pro ala val leu gln arg
241/81                                271/91
gaa gac atc gac aca gcg acg gag gtg ccg gcg ccg gtg agc gcg ttg ccg gag gcc gcg
glu asp ile asp thr ala thr glu val pro ala pro val ser ala leu arg glu ala ala
lys thr ser thr gln arg arg arg cys arg arg arg OPA ala arg cys gly arg pro arg
arg his arg his ser asp gly gly ala gly ala gly glu arg val ala gly gly arg val
301/101                                331/111
tct gac gcg cac gct gcc ttg gtg gtc acg ccg gaa tac aac ggc agc att ccg gcc gtg
ser asp ala his ala ala leu val val thr pro glu tyr asn gly ser ile pro ala val
leu thr arg thr leu pro trp trp ser arg arg asn thr thr ala ala phe arg pro OPA
OPA arg ala arg cys leu gly gly his ala gly ile gln arg gln his ser gly arg asp
361/121                                391/131
atc aag aac gcg atc gac tgg ctg tcc agg cca ttc ggc gat ggc gcg ttg aag gac aag
ile lys asn ala ile asp trp leu ser arg pro phe gly asp gly ala leu lys asp lys
ser arg thr arg ser thr gly cys pro gly his ser ala met ala arg OPA arg thr ser
gln glu arg asp arg leu ala val gln ala ile arg arg trp arg val glu gly gln ala
421/141                                451/151
ccg ttg gcc gtg atc ggc ggc tcc atg ggc cgc tac ggc ggg gta tgg gcg cac gac gag
pro leu ala val ile gly gly ser met gly arg tyr gly gly val trp ala his asp glu
arg trp pro OPA ser ala ala pro trp ala ala thr ala gly tyr gly arg thr thr arg
val gly arg asp arg arg leu his gly pro leu arg arg gly met gly ala arg arg asp
481/161                                511/171
act cgc aag tcg ttc agc atc gct ggc acg ccg gtg gtc gat gcg atc aaa ctg tcg gtg
thr arg lys ser phe ser ile ala gly thr arg val val asp ala ile lys leu ser val
leu ala ser arg ser ala ser leu ala arg gly trp ser met arg ser asn cys arg cys
ser gln val val gln his arg trp his ala gly gly arg cys asp gln thr val gly ala
541/181                                571/191
ccg ttc caa act ctg ggc aag tcg gtc gcg gac gac gcc ggg ctg gcg gcg aat gtg cgc
pro phe gln thr leu gly lys ser val ala asp asp ala gly leu ala ala asn val arg
arg ser lys leu trp ala ser arg ser arg thr thr pro gly trp arg arg met cys ala
val pro asn ser gly gln val gly arg gly arg arg ala gly gly glu cys ala arg
601/201                                631/211
gac gcc gtc ggc aac ttg gcc gct gag gtc ggc tga tcc ctg ggc cga ggc ggg tca gcc
asp ala val gly asn leu ala ala glu val gly OPA ser leu gly arg gly gly ser ala
thr pro ser ala thr trp pro leu arg ser ala asp pro trp ala glu ala gly gln pro
arg arg arg gln leu gly arg OPA gly arg leu ile pro gly pro arg arg val ser gln
661/221                                691/231
aat agc ggc tcc atc ggc ttt gct ggt agc ggt tcg gcg gga agc tag ccg cga cgt tgt
asn ser gly ser ile gly phe ala gly ser gly ser ala gly ser AMB arg arg arg cys
ile ala ala pro ser ala leu leu val ala val arg arg glu ala ser gly asp val val
AMB arg leu his arg leu cys trp AMB arg phe gly gly lys leu ala ala thr leu ser

```

SEQ ID No.14Q

FIGURE 14Q

REPLACEMENT SHEET (RULE 26)

721/241
 cgg tgg ccg gtg ata tat tgg gtc aga cgg gta tgg cgg cgg ctg agg tga tct gcg aca
 arg trp pro val ile tyr trp val arg val trp arg arg leu arg OPA ser ala thr
 gly gly arg OPA tyr ile gly ser asp gly tyr gly gly gly OPA gly asp leu arg his
 val ala gly asp ile leu gly gln thr gly met ala ala ala glu val ile cys asp thr
 781/261
 cgc cgc cgc ggt gct cga gcc agg ctt acg acc agg gaa ttt cga aaa tgt tat tca gaa
 arg arg arg gly ala arg ala arg leu thr thr arg glu phe arg lys cys tyr ser glu
 ala ala ala val leu glu pro gly leu arg pro gly asn phe glu asn val ile gln asn
 pro pro arg cys ser ser gln ala tyr asp gln gly ile ser lys met leu phe arg thr
 841/281
 cat ctt gta tct ctt ctc cgt gcc acc ccc tag gtg tag tgt ttt cga gta ccg gca gat
 his leu val ser leu leu arg ala thr pro AMB val AMB cys phe arg val pro ala asp
 ile leu tyr leu phe ser val pro pro arg cys ser val phe glu tyr arg gln ile
 ser cys ile ser ser pro cys his pro leu gly val val phe ser ser thr gly arg ser
 901/301
 ccc agg ttc acc agg tct cac cag atc cac ggg gcg cga tga act tcc cgg cat cgg cat
 pro arg phe thr arg ser his gln ile his gly ala arg OPA thr ser arg his arg his
 pro gly ser pro gly leu thr arg ser thr gly arg asp glu leu pro gly ile gly ile
 gln val his gln val ser pro asp pro arg gly ala met asn phe pro ala ser ala ser
 961/321
 cgc cag gtc gac gga cgt ggt cgc gct atg acg gga atc tgg agc ctt gtc ggg ccg ctc
 arg gln val asp gly arg gly arg ala met thr gly ile trp ser leu val gly pro leu
 ala arg ser thr asp val val ala leu OPA arg glu ser gly ala leu ser gly arg ser
 pro gly arg arg thr trp ser arg tyr asp gly asn leu glu pro cys arg ala ala gln
 1021/341
 aac ata tcg aag atg cac tac ttg agt cgt tgc cag atc ctg tca gat tcc cga ttt ccg
 asn ile ser lys met his tyr leu ser arg cys gln ile leu ser asp ser arg phe pro
 thr tyr arg arg cys thr thr OPA val val ala arg ser cys gln ile pro asp phe arg
 his ile glu asp ala leu leu glu ser leu pro asp pro val arg phe pro ile ser ala
 1081/361
 caa agg agc ggt acg ccc atg acc gtg acc gtt tac act aa
 gln arg ser gly thr pro met thr val thr val tyr thr
 lys gly ala val arg pro OPA pro OPA pro phe thr leu
 lys glu arg tyr ala his asp arg asp arg leu his OCH

SEQ ID No.14Q(continued)

FIGURE 14Q(continued)

1/1
 CAA GCC CGG CCG CGA CTG TTT GCC GTT TTG GGG CTC CTA CCA GAA CAC CAC CTG GCG GCC
 gln ala arg pro arg leu phe ala val leu gly leu leu pro glu his his leu ala ala
 61/21
 GCG CAC CAT GGT GTG CAC CAG TTG CGA TCG GTT CCT CCC GCG CGC GGG CGG CGA CGA CGT
 ala his his gly val his gln leu arg ser val pro pro ala arg gly arg arg arg arg
 121/41
 CGA TGC CCG CGC CCC GGC GGC GCA GCT GCG TAG CTC GAC CCG GTC GAC GAC GAC GGG GTC
 arg cys pro arg pro gly gly ala ala ala AMB leu asp pro val asp asp asp gly val
 181/61
 GGC GGA CCA GTC GGC GAT GTC GAG GCG ATG GCA ATA CAG CGC CTT GGT GCG CGG CCA CAC
 gly gly pro val gly asp val glu ala met ala ile gln arg leu gly ala arg pro his
 241/81
 GTC TGA GGT GGC GAA GAC CAG TCC CGC GCC CAC CGG CAG CCG GAT CCG GAT ACG CGG TAC
 val OPA gly gly glu asp gln ser arg ala his arg gln pro asp pro asp thr arg tyr

SEQ ID No.15A

FIGURE 15A

REPLACEMENT SHEET (RULE 26)

50/185

32/11
AAG CCC GGC CGC GAC TGT TTG CCG TTT TGG GGC TCC TAC CAG AAC ACC ACC TGG CGG CCG
lys pro gly arg asp cys leu pro phe trp gly ser tyr gln asn thr thr trp arg pro
62/21
CGC ACC ATG GTG TGC ACC AGT TGC GAT CGG TTC CTC CCG CGC GCG GGC GGC GAC GAC GTC
arg thr met val cys thr ser cys asp arg phe leu pro arg ala gly gly asp asp val
122/41
GAT GCC CGC GCC CCG GCG GCG CAG CTG CGT AGC TCG ACC CGG TCG ACG ACG ACG GGG TCG
asp ala arg ala pro ala ala gln leu arg ser ser thr arg ser thr thr thr gly ser
182/61
GCG GAC CAG TCG GCG ATG TCG AGG CGA TGG CAA TAC AGC GCC TTG GTG CGC GGC CAC ACG
ala asp gln ser ala met ser arg arg trp gln tyr ser ala leu val arg gly his thr
242/81
TCT GAG GTG GCG AAG ACC AGT CCC GCG CCC ACC GGC AGC CGG ATC CGG ATA CGC GGT AC
ser glu val ala lys thr ser pro ala pro thr gly ser arg ile arg ile arg gly

SEQ ID No.15B

FIGURE 15B

33/11
AGC CCG GCC GCG ACT GTT TGC CGT TTT GGG GCT CCT ACC AGA ACA CCA CCT GGC GGC CGC
ser pro ala ala thr val cys arg phe gly ala pro thr arg thr pro pro gly gly arg
63/21
GCA CCA TGG TGT GCA CCA GTT GCG ATC GGT TCC TCC CGC GCG CGG GCG GCG ACG ACG TCG
ala pro trp cys ala pro val ala ile gly ser ser arg ala arg ala ala thr thr ser
123/41
ATG CCC GCG CCC CGG CGG CGC AGC TGC GTA GCT CGA CCC GGT CGA CGA CGA CGG GGT CGG
met pro ala pro arg arg arg ser cys val ala arg pro gly arg arg arg arg gly arg
183/61
CGG ACC AGT CGG CGA TGT CGA GGC GAT GGC AAT ACA GCG CCT TGG TGC GCG GCC ACA CGT
arg thr ser arg arg cys arg gly asp gly asn thr ala pro trp cys ala ala thr arg
243/81
CTG AGG TGG CGA AGA CCA GTC CCG CGC CCA CCG GCA GCC GGA TCC GGA TAC GCG GTA C
leu arg trp arg arg pro val pro arg pro pro ala ala gly ser gly tyr ala val

SEQ ID No.15C

FIGURE 15C

part of the nucleotide sequence of seq15A

1/1	31/11
GGC GGC CGC GCG CCA TGG TGT GCA CCA GTT	GCG ATC GGT TCT CCC GCG CGC GGG CGG CGA
gly gly arg ala pro trp cys ala pro val	ala ile gly ser pro ala arg gly arg arg
61/21	91/31
CGA CGT CGA TGG CCG CGC CCC GGC GGC TGC	AGC TGC GTA GCT CGA CCC GGT CGA CGA CGA
arg arg arg trp pro arg pro gly gly cys	ser cys val ala arg pro gly arg arg arg
121/41	151/51
CGG GGT CGG CGG GCC AGT CGG CGA TGT CGA	GGC GAT GGC AAT ACA GCG CCT TGG TGC GCG
arg gly arg arg ala ser arg arg cys arg	gly asp gly asn thr ala pro trp cys ala
181/61	211/71
GCC ACA CGT CTG AGG TGG CGA AGA CCA GTC	CCG CGC CCA CCG GCA GCC GGA TC
ala thr arg leu arg trp arg arg pro val	pro arg pro pro ala ala gly

SEQ ID No.15A'

FIGURE 15A'

1/1	31/11
GCG GCC GCG CGC CAT GGT GTG CAC CAG TTG	CGA TCG GTT CTC CCG CGC GCG GGC GGC GAC
ala ala ala arg his gly val his gln leu	arg ser val leu pro arg ala gly gly asp
61/21	91/31
GAC GTC GAT GGC CGC GCC CCG GCG GCT GCA	GCT GCG TAG CTC GAC CCG GTC GAC GAC GAC
asp val asp gly arg ala pro ala ala ala	ala ala AMB leu asp pro val asp asp asp
121/41	151/51
GGG GTC GGC GGG CCA GTC GGC GAT GTC GAG	GCG ATG GCA ATA CAG CGC CTT GGT GCG CGG
gly val gly gly pro val gly asp val glu	ala met ala ile gln arg leu gly ala arg
181/61	211/71
CCA CAC GTC TGA GGT GGC GAA GAC CAG TCC	CGC GCC CAC CGG CAG CCG GAT C
pro his val OPA gly gly glu asp gln ser	arg ala his arg gln pro asp

SEQ ID No.15B'

FIGURE 15B'

1/1	31/11
TGG CGG CCG CGC GCC ATG GTG TGC ACC AGT	TGC GAT CGG TTC TCC CGC GCG CGG GCG GCG
trp arg pro arg ala met val cys thr ser	cys asp arg phe ser arg ala arg ala ala
61/21	91/31
ACG ACG TCG ATG GCC GCG CCC CGG CGG CTG	CAG CTG CGT AGC TCG ACC CGG TCG ACG ACG
thr thr ser met ala ala pro arg arg leu	gln leu arg ser ser thr arg ser thr thr
121/41	151/51
ACG GGG TCG GCG GGC CAG TCG GCG ATG TCG	AGG CGA TGG CAA TAC AGC GCC TTG GTG CGC
thr gly ser ala gly gln ser ala met ser	arg arg trp gln tyr ser ala leu val arg
181/61	211/71
GGC CAC ACG TCT GAG GTG GCG AAG ACC AGT	CCC GCG CCC ACC GGC AGC CGG ATC
gly his thr ser glu val ala lys thr ser	pro ala pro thr gly ser arg ile

SEQ ID No.15C'

FIGURE 15C'

ORF containing Seq15A' according to Cole et al. (Nature 393:537-544)

1/1	31/11
taa ggt ccg cca acg ctt tac gct cga cgg	ccg cca cga gtt ggc cgg cca ctt tca ggc
OCH gly pro pro thr leu tyr ala arg arg	pro pro arg val gly arg pro leu ser gly
61/21	91/31
cgt agt cgc cgc agg gca ggg ctt ccc gcg	tcg tct tcg cgg gtt tgt cgg caa agg tgt
arg ser arg arg arg ala gly leu pro ala	ser ser ser arg val cys arg gln arg cys
121/41	151/51
agg ggt agc gtt cgt ggg cgt cga cga cga	tgt gca gct cgg gga tgc cgg cgg cgc ggg
arg gly ser val arg gly arg arg arg arg	cys ala ala arg gly cys arg arg arg gly
181/61	211/71
cgg tgg ggg tgc gca cgc ccg gcc gcg act	ggt tgc gcg ttt tgg ggc tct gcc aga aca
arg trp gly cys ala arg pro ala ala thr	val cys ala phe trp gly ser ala arg thr
241/81	271/91
cca cct ggc ggc cgc gcg cca tgg tgt gca	cca gtt gcg atc ggt tct ccc gcg cgc ggg
pro pro gly gly arg ala pro trp cys ala	pro val ala ile gly ser pro ala arg gly
301/101	331/111
cgg cga cga cgt cga tgg ccg cgc ccc ggc	ggc tgc agc tgc gta gct cga ccc ggt cga
arg arg arg arg arg trp pro arg pro gly	gly cys ser cys val ala arg pro gly arg
361/121	391/131
cga cga cgg ggt cgg cgg gcc agt cgg cga	tgt cga ggc gat ggc aat aca gcg cct tgg
arg arg arg gly arg arg ala ser arg arg	cys arg gly asp gly asn thr ala pro trp
421/141	451/151
tgc gcg gcc aca cgt ctg agg tgg cga aga	cca gtc ccg cgc cca ccg gca gcc gga tca
cys ala ala thr arg leu arg trp arg arg	pro val pro arg pro pro ala ala gly ser
481/161	511/171
ggt agg gca ggc gcg agt ctt cag cgg ggt	tgg cgg cga cga gca gct cca cag agt gtg
gly arg ala gly ala ser leu gln arg gly	trp arg arg arg ala ala pro gln ser val
541/181	571/191
agg gta cgg gcg gcg tac ggc aac ggt gaa	gca ggc act ccg acg aac cca tcg tca cgt
arg val arg ala ala tyr gly asn gly glu	ala gly thr pro thr asn pro ser ser arg
601/201	
cga agg ggc agg tga	
arg arg gly arg OPA	

SEQ ID No.15F

FIGURE 15F

53/185

R:Rv2530c predicted according to Cole et al. (Nature 393:537-544) and which may be in phase with SEQ15A

```

1/1                               31/11
gtg acg gca ctg ctc gat gtc aat gtg ctg atc gcg ctg ggc tgg ccg aat cac gtt cac
val thr ala leu leu asp val asn val leu ile ala leu gly trp pro asn his val his
61/21                             91/31
cat gcg gcc gcg cag cga tgg ttc acg cag ttc tcc tcg aat ggg tgg gcc acc acg ccg
his ala ala ala gln arg trp phe thr gln phe ser ser asn gly trp ala thr thr pro
121/41                           151/51
atc acc gag gca ggg tat gtc cga att tca agc aat cgc agt gtg atg cag gtg tcg acc
ile thr glu ala gly tyr val arg ile ser ser asn arg ser val met gln val ser thr
181/61                           211/71
acg ccg gct atc gcg atc gct cag ttg gcg gcg atg act tct ctt gcc ggg cac acg ttt
thr pro ala ile ala ile ala gln leu ala ala met thr ser leu ala gly his thr phe
241/81                           271/91
tgg cct gac gat gtg cca ctg atc gtt ggg agc gcc gcc gat cgc gat gcg gtg tcc aac
trp pro asp asp val pro leu ile val gly ser ala gly asp arg asp ala val ser asn
301/101                          331/111
cac cgt cgg gtc acc gac tgc cat ctc atc gcc ttg gcc gcg cgc tac ggg gcc cgg ttg
his arg arg val thr asp cys his leu ile ala leu ala ala arg tyr gly gly arg leu
361/121                          391/131
gtc aca ttc gat gcc gca ctg gcc gat tca gca tcc gca gcc ctc gtc gag gtg ttg tag
val thr phe asp ala ala leu ala asp ser ala ser ala gly leu val glu val leu AMB

```

SEQ ID No.15R

FIGURE 15R

Seq15P: ORF according to Cole et al. (Nature 393:537-544) containing Rv2530c

```

1/1                               31/11
tga tgt tcc gcc gga tgc gcc gac ggt gac ttc cga gga tgt cgt ccg cgc gct cga gga
OPA cys ser ala gly cys ala asp gly asp phe arg gly cys arg pro arg ala arg gly
61/21                             91/31
cga cgt gtg acg gca ctg ctc gat gtc aat gtg ctg atc gcg ctg ggc tgg ccg aat cac
arg arg val thr ala leu leu asp val asn val leu ile ala leu gly trp pro asn his
121/41                           151/51
gtt cac cat gcg gcc gcg cag cga tgg ttc acg cag ttc tcc tcg aat ggg tgg gcc acc
val his his ala ala ala gln arg trp phe thr gln phe ser ser asn gly trp ala thr
181/61                           211/71
acg ccg atc acc gag gca ggg tat gtc cga att tca agc aat cgc agt gtg atg cag gtg
thr pro ile thr glu ala gly tyr val arg ile ser ser asn arg ser val met gln val
241/81                           271/91
tcg acc acg ccg gct atc gcg atc gct cag ttg gcg gcg atg act tct ctt gcc ggg cac
ser thr thr pro ala ile ala ile ala gln leu ala ala met thr ser leu ala gly his
301/101                          331/111
acg ttt tgg cct gac gat gtg cca ctg atc gtt ggg agc gcc gcc gat cgc gat gcg gtg
thr phe trp pro asp asp val pro leu ile val gly ser ala gly asp arg asp ala val
361/121                          391/131
tcc aac cac cgt cgg gtc acc gac tgc cat ctc atc gcc ttg gcc gcg cgc tac ggg gcc
ser asn his arg arg val thr asp cys his leu ile ala leu ala ala arg tyr gly gly
421/141                          451/151
cgg ttg gtc aca ttc gat gcc gca ctg gcc gat tca gca tcc gca gcc ctc gtc gag gtg
arg leu val thr phe asp ala ala leu ala asp ser ala ser ala gly leu val glu val
481/161
ttg tag
leu AMB

```

SEQ ID No.15P

FIGURE 15P

REPLACEMENT SHEET (RULE 26)

Fragment containing Seq15P' and Seq 15F'

1/1 31/11
 tga tgt tcc gcc gga tgc gcc gac ggt gac ttc cga gga tgt cgt ccg cgc gct cga gga
 OPA cys ser ala gly cys ala asp gly asp phe arg gly cys arg pro arg ala arg gly
 asp val pro pro asp ala pro thr val thr ser glu asp val val arg ala leu glu asp
 Met phe arg arg met arg arg arg OPA leu pro arg met ser ser ala arg ser arg thr
 61/21 91/31
 cga cgt gtg acg gca ctg ctc gat gtc aat gtg ctg atc gcg ctg ggc tgg ccg aat cac
 arg arg val thr ala leu leu asp val asn val leu ile ala leu gly trp pro asn his
 asp val OPA arg his cys ser met ser met cys OPA ser arg trp ala gly arg ile thr
 thr cys asp gly thr ala arg cys gln cys ala asp arg ala gly leu ala glu ser arg
 121/41 151/51
 gtt cac cat gcg gcc gcg cag cga tgg ttc acg cag ttc tcc tcg aat ggg tgg gcc acc
 val his his ala ala ala gln arg trp phe thr gln phe ser ser asn gly trp ala thr
 phe thr met arg pro arg ser asp gly ser arg ser ser pro arg met gly gly pro pro
 ser pro cys gly arg ala ala met val his ala val leu leu glu trp val gly his his
 181/61 211/71
 acg ccg atc acc gag gca ggg tat gtc cga att tca agc aat cgc agt gtg atg cag gtg
 thr pro ile thr glu ala gly tyr val arg ile ser ser asn arg ser val met gln val
 arg arg ser pro arg gln gly met ser glu phe gln ala ile ala val OPA cys arg cys
 ala asp his arg gly arg val cys pro asn phe lys gln ser gln cys asp ala gly val
 241/81 271/91
 tcg acc acg ccg gct atc gcg atc gct cag ttg gcg gcg atg act tct ctt gcc ggg cac
 ser thr thr pro ala ile ala ile ala gln leu ala ala met thr ser leu ala gly his
 arg pro arg arg leu ser arg ser leu ser trp arg arg OPA leu leu leu pro gly thr
 asp his ala gly tyr arg asp arg ser val gly gly asp asp phe ser cys arg ala his
 301/101 331/111
 acg ttt tgg cct gac gat gtg cca ctg atc gtt ggg agc gcc ggc gat cgc gat gcg gtg
 thr phe trp pro asp asp val pro leu ile val gly ser ala gly asp arg asp ala val
 arg phe gly leu thr met cys his OPA ser leu gly ala pro ala ile ala met arg cys
 val leu ala OPA arg cys ala thr asp arg trp glu arg arg arg ser arg cys gly val
 361/121 391/131
 tcc aac cac cgt cgg gtc acc gac tgc cat ctc atc gcc ttg gcc gcg cgc tac ggg gcc
 ser asn his arg arg val thr asp cys his leu ile ala leu ala ala arg tyr gly gly
 pro thr thr val gly ser pro thr ala ile ser ser pro trp pro arg ala thr gly ala
 gln pro pro ser gly his arg leu pro ser his arg leu gly arg ala leu arg gly pro
 421/141 451/151
 cgg ttg gtc aca ttc gat gcc gca ctg gcc gat tca gca tcc gca ggc ctc gtc gag gtg
 arg leu val thr phe asp ala ala leu ala asp ser ala ser ala gly leu val glu val
 gly trp ser his ser met pro his trp pro ile gln his pro gln ala ser ser arg cys
 val gly his ile arg cys arg thr gly arg phe ser ile arg arg pro arg arg gly val
 481/161 511/171
 ttg tag tca ccg ggg atg gcc ggc tgc cca gcc ctg cag gat ctg ccg gcg cag gcc ccc
 leu AMB ser pro gly met gly gly ser pro gly leu gln asp leu arg ala gln ala pro
 cys ser his arg gly trp ala ala arg gln ala cys arg ile cys gly arg arg arg pro
 val val thr gly asp gly arg leu ala arg pro ala gly ser ala gly ala gly ala pro
 541/181 571/191
 ccg gtc gga cac ccg cag gcc gac gct ttt gcc cca cgc gcg cag ctc gcc gct gct ggg
 pro val gly his arg gln ala asp ala phe gly pro arg ala gln leu gly ala ala gly
 arg ser asp thr gly arg pro thr leu leu ala his ala arg ser ser ala leu leu gly
 gly arg thr pro ala gly arg arg phe trp pro thr arg ala ala arg arg cys trp ala
 601/201 631/211
 ctc ggg ctc gcc gcc agc ccg ctc gaa aac cgt ggt gcc gtc gcc atc gtc gac gaa cca
 leu gly leu gly gly ser arg leu glu asn arg gly val gly ile val asp glu pro
 ser gly ser ala ala gly ser lys thr val val ala ser ala ser ser thr asn gln
 arg ala arg arg gln pro ala arg lys pro trp trp arg arg his arg arg arg thr arg

SEQ ID No.15Q

FIGURE 15Q

661/221 691/231
 ggt gag ggc ggc ggc tag ata gcg gta ggt gta ttc ctg ggc gag ctt gcg ggt ttg gca
 gly glu gly gly gly AMB ile ala val gly val phe leu gly glu leu ala gly leu ala
 val arg ala ala ala arg AMB arg AMB val tyr ser trp ala ser leu arg val trp gln
 OPA gly arg arg leu asp ser gly arg cys ile pro gly arg ala cys gly phe gly arg
 721/241 751/251
 gaa cac gat cgg cac gtt ggg aaa gcc gat ctg caa ttc ggc cag ccc atc gcc gat cgc
 glu his asp arg his val gly lys ala asp leu gln phe gly gln pro ile gly asp arg
 asn thr ile gly thr leu gly lys pro ile cys asn ser ala ser pro ser ala ile ala
 thr arg ser ala arg trp glu ser arg ser ala ile arg pro ala his arg arg ser pro
 781/261 811/271
 cgt cgg gcg ggc gaa gga gtg cgc gaa gat ctg caa gta gcg gtc ctc gac cac cac ggc
 arg arg ala gly glu gly val arg glu asp leu arg val ala val leu asp his his gly
 val gly arg ala lys glu cys ala lys ile ser glu AMB arg ser ser thr thr thr ala
 ser gly gly arg arg ser ala arg arg ser pro ser ser gly pro arg pro pro arg arg
 841/281 871/291
 ggc cgg tgg cag cgc ggc cag ttc ggt cag ttg gta ttt cag gtt gcc gtt cag cac gcc
 gly pro trp gln arg gly gln phe gly gln leu val phe gln val ala val gln his ala
 ala arg gly ser ala ala ser ser val ser trp tyr phe arg leu pro phe ser thr pro
 pro val ala ala arg pro val arg ser val gly ile ser gly cys arg ser ala arg gln
 901/301 931/311
 aga agt aag gtc cgc caa cgc ttt acg ctc gac gcc cgc cac gag ttg gcc ggc cac ttt
 arg ser lys val arg gln arg phe thr leu asp gly arg his glu leu ala gly his phe
 glu val arg ser ala asn ala leu arg ser thr ala ala thr ser trp pro ala thr phe
 lys OCH gly pro pro thr leu tyr ala arg arg pro pro arg val gly arg pro leu ser
 961/321 991/331
 cag gcc gta gtc gcc gca ggg cag ggc ttc ccg cgt ctt cgc ggg ttt gtc gcc aaa
 gln ala val val ala ala gly gln gly phe pro arg arg leu arg gly phe val gly lys
 arg pro AMB ser pro gln gly arg ala ser arg val val phe ala gly leu ser ala lys
 gly arg ser arg arg arg ala gly leu pro ala ser ser arg val cys arg gln arg
 1021/341 1051/351
 ggt gta ggg gta gcg ttc gtg ggc gtc gac gat gtg cag ctc ggg gat gcc ggc ggc
 gly val gly val ala phe val gly val asp asp val gln leu gly asp ala gly gly
 val AMB gly AMB arg ser trp ala ser thr thr met cys ser ser gly met pro ala ala
 cys arg gly ser val arg gly arg arg arg arg cys ala ala arg gly cys arg arg arg
 1081/361 1111/371
 gcg ggc ggt ggg ggt gcg cac gcc cgg ccg cga ctg ttt gcg cgt ttt ggg gct ctg cca
 ala gly gly gly gly ala his ala arg pro arg leu phe ala arg phe gly ala leu pro
 arg ala val gly val arg thr pro gly arg asp cys leu arg val leu gly leu cys gln
 gly arg trp gly cys ala arg pro ala ala thr val cys ala phe trp gly ser ala arg
 1141/381 1171/391
 gaa cac cac ctg gcg gcc gcg cgc cat ggt gtg cac cag ttg cga tcg gtt ctc ccg cgc
 glu his his leu ala ala ala arg his gly val his gln leu arg ser val leu pro arg
 asn thr thr trp arg pro arg ala met val cys thr ser cys asp arg phe ser arg ala
 thr pro pro gly gly arg ala pro trp cys ala pro val ala ile gly ser pro ala arg
 1201/401 1231/411
 gcg ggc ggc gac gac gtc gat ggc cgc gcc ccg gcg gct gca gct gcg tag ctc gac ccg
 ala gly gly asp asp val asp gly arg ala pro ala ala ala ala AMB leu asp pro
 arg ala ala thr thr ser met ala ala pro arg arg leu gln leu arg ser ser thr arg
 gly arg arg arg arg arg trp pro arg pro gly gly cys ser cys val ala arg pro gly
 1261/421 1291/431
 gtc gac gac gac ggg gtc ggc ggg cca gtc gcc gat gtc gag gcg atg gca ata cag cgc
 val asp asp asp gly val gly gly pro val gly asp val glu ala met ala ile gln arg
 ser thr thr thr gly ser ala gly gln ser ala met ser arg arg trp gln tyr ser ala
 arg arg arg arg gly arg arg ala ser arg arg cys arg gly asp gly asn thr ala pro

SEQ ID No.15Q (continued 1)

FIGURE 15Q (continued 1)

1321/441
 ctt ggt gcg cgg cca cac gtc tga ggt ggc gaa gac cag tcc cgc gcc cac cgg cag ccg
 leu gly ala arg pro his val OPA gly gly glu asp gln ser arg ala his arg gln pro
 leu val arg gly his thr ser glu val ala lys thr ser pro ala pro thr gly ser arg
 trp cys ala ala thr arg leu arg trp arg pro val pro arg pro pro ala ala gly
 1381/461
 gat cag gta ggg cag gcg cga gtc ttc agc ggg gtt ggc gcc gac gag cag ctc cac aga
 asp gln val gly gln ala arg val phe ser gly val gly gly asp glu gln leu his arg
 ile arg AMB gly arg arg glu ser ser ala gly leu ala ala thr ser ser ser thr glu
 ser gly arg ala gly ala ser leu gln arg gly trp arg arg arg ala ala pro gln ser
 1441/481
 gtg tga ggg tac ggg cgg cgt acg gca acg gtt aag cag gca ctc cga cga acc cat cgt
 val OPA gly tyr gly arg arg thr ala thr val lys gln ala leu arg arg thr his arg
 cys glu gly thr gly gly val arg gln arg OPA ser arg his ser asp glu pro ile val
 val arg val arg ala ala tyr gly asn gly glu ala gly thr pro thr asn pro ser ser
 1501/501
 cac gtc gaa ggg gca ggt ga
 his val glu gly ala gly
 thr ser lys gly gln val
 arg arg arg gly arg OPA

SEQ ID No.15Q (continued 2)

FIGURE 15Q (continued (2))

31/11
 TGC GCA TGC CGA CCA GTG TGG TTG GCC GGA GTT CGT TTG TTC GCG ATT GCC TCA ACG ATT
 cys ala cys arg pro val trp leu ala gly val arg leu phe ala ile ala ser thr ile
 61/21
 CGA TAT AAC CAC TCT AGT CAC ATC AAC CAC ACT CGT ACC ATC GAG CGT GTG GGT TCA TGC
 arg tyr asn his ser ser his ile asn his thr arg thr ile glu arg val gly ser cys
 121/41
 CAT GCA TTC GCG ACC GCG GGA GCC GGC GAA CCC GGC GCC ACA CAT AAT CCA GAT TGA GGA
 his ala phe ala thr ala gly ala gly glu pro gly ala thr his asn pro asp OPA gly
 181/61
 GAC TTC CGT GCC GAA CCG ACG CCG ACG CAA GCT TTC GAC AGC CAT GAG CGC GGT CGC CGC
 asp phe arg ala glu pro thr pro thr gln ala phe asp ser his glu arg gly arg arg
 241/81
 CCT GGC AGT TGC AAG TCC TTG TGC ATA TTT TCT TGT CTA CGA ATC AAC CGA AAC GAC CGA
 pro gly ser cys lys ser leu cys ile phe ser cys leu arg ile asn arg asn asp arg
 301/101
 GCG GCC CGA GCA CCA TGA ATT CAA GCA GGC GGC GGT GTT GAC CGA CCT GCC CGG CGA GCT
 ala ala arg ala pro OPA ile gln ala gly gly gly val asp arg pro ala arg arg ala
 361/121
 GAT GTC CGC GCT ATC GCA GGG GTT GTC CCA GTT CGG GAT C
 asp val arg ala ile ala gly val val pro val arg asp

SEQ ID No.16A

FIGURE 16A

57/185

32/11
 GCG CAT GCC GAC CAG TGT GGT TGG CCG GAG TTC GTT TGT TCG CGA TTG CCT CAA CGA TTC
 ala his ala asp gln cys gly trp pro glu phe val cys ser arg leu pro gln arg phe
 62/21 92/31
 GAT ATA ACC ACT CTA GTC ACA TCA ACC ACA CTC GTA CCA TCG AGC GTG TGG GTT CAT GCC
 asp ile thr thr leu val thr ser thr thr leu val pro ser ser val trp val his ala
 122/41 152/51
 ATG CAT TCG CGA CCG CGG GAG CCG GCG AAC CCG GCG CCA CAC ATA ATC CAG ATT GAG GAG
 met his ser arg pro arg glu pro ala asn pro ala pro his ile ile gln ile glu glu
 182/61 212/71
 ACT TCC GTG CCG AAC CGA CGC CGA CGC AAG CTT TCG ACA GCC ATG AGC GCG GTC GCC GCC
 thr ser val pro asn arg arg arg arg lys leu ser thr ala met ser ala val ala ala
 242/81 272/91
 CTG GCA GTT GGA AGT CCT TGT GCA TAT TTT CTT GTC TAC GAA TCA ACC GAA ACG ACC GAG
 leu ala val ala ser pro cys ala tyr phe leu val tyr glu ser thr glu thr thr glu
 302/101 332/111
 CGG CCC GAG CAC CAT GAA TTC AAG CAG GCG GCG GTG TTG ACC GAC CTG CCC GGC GAG CTG
 arg pro glu his his glu phe lys gln ala ala val leu thr asp leu pro gly glu leu
 362/121 392/131
 ATG TCC GCG CTA TCG CAG GGG TTG TCC CAG TCC GGG ATC
 met ser ala leu ser gln gly leu ser gln phe gly ile

SEQ ID No.16B

FIGURE 16B

33/11
 CGC ATG CCG ACC AGT GTG GTT GGC CGG AGT TCG TTT GTT CGC GAT TGC CTC AAC GAT TCG
 arg met pro thr ser val val gly arg ser ser phe val arg asp cys leu asn asp ser
 63/21 93/31
 ATA TAA CCA CTC TAG TCA CAT CAA CCA CAC TCG TAC CAT CGA GCG TGT GGG TTC ATG CCA
 ile OCH pro leu AMB ser his gln pro his ser tyr his arg ala cys gly phe met pro
 123/41 153/51
 TGC ATT CGC GAC CGC GGG AGC CGG CGA ACC CGG CGC CAC ACA TAA TCC AGA TTG AGG AGA
 cys ile arg asp arg gly ser arg arg thr arg arg his thr OCH ser arg leu arg arg
 183/61 213/71
 CTT CCG TGC CGA ACC GAC GCC GAC GCA AGC TTT CGA CAG CCA TGA GCG CGG TCG CCG CCC
 leu pro cys arg thr asp ala asp ala ser phe arg gln pro OPA ala arg ser pro pro
 243/81 273/91
 TGG CAG TTG CAA GTC CTT GTG CAT ATT TTC TTG TCT ACG AAT CAA CCG AAA CGA CCG AGC
 trp gln leu gln val leu val his ile phe leu ser thr asn gln pro lys arg pro ser
 303/101 333/111
 GGC CCG AGC ACC ATG AAT TCA AGC AGG CGG CGG TGT TGA CCG ACC TGC CCG GCG AGC TGA
 gly pro ser thr met asn ser ser arg arg arg cys OPA pro thr cys pro ala ser OPA
 363/121 393/131
 TGT CCG CGC TAT CGC AGG GGT TGT CCC AGT TCG GGA TC
 cys pro arg tyr arg arg gly cys pro ser ser gly

SEQ ID No.16C

FIGURE 16C

31/11
 GCG GGC CAC CGA TCA GTC GAT CGG GTG GTT TCC GCT CCA TCA GCC CGG AAT TGA GGT GCC
 ala gly his arg ser val asp arg val val ser ala pro ser ala arg asn OPA gly ala
 61/21
 GCA GTG ACG ACA CCA GCG CAG GAC GCG CCG TTG GTG TTT CCC TCT GTT GCT TTC CCG TCC
 ala val thr thr pro ala gln asp ala pro leu val phe pro ser val ala phe pro ser
 121/41
 GGC TCG CCT TTT TTT CAT CAA CGT TGG ACT GCC GCA GTG GCG ATG TTG GTC GCC GGC GTG
 gly ser pro phe phe his gln arg trp thr ala ala val ala met leu val ala gly val
 181/61
 TTC GGT CAC CTG ACG GTC GGG ATG TTC CTT GGG TCT CGG GTT GCT GCT GGG TTT GCT CAA
 phe gly his leu thr val gly met phe leu gly ser arg val ala ala gly phe ala gln
 241/81
 TGC CCT GCT GGT GCG GCG TTC GGC CGA GTC GAT CAC CGC CAA AGA GCA CCC GTT AAA ACG
 cys pro ala gly ala ala phe gly arg val asp his arg gln arg ala pro val lys thr
 301/101
 GTC GAT GGC CCT CAA CTC GGC ATC GCG ACT GGC GAT TAT CAC CAT GCC TCG GGC TGA TC
 val asp gly pro gln leu gly ile ala thr gly asp tyr his his ala ser gly OPA

SEQ ID No.17A

FIGURE 17A

32/11
 CGG GCC ACC GAT CAG TCG ATC GGG TGG TTT CCG CTC CAT CAG CCC GGA ATT GAG GTG CCG
 arg ala thr asp gln ser ile gly trp phe pro leu his gln pro gly ile glu val pro
 62/21
 CAG TGA CGA CAC CAG CGC AGG ACG CGC CGT TGG TGT TTC CCT CTG TTG CTT TCC CGT CCG
 gln OPA arg his gln arg arg thr arg arg trp cys phe pro leu leu leu ser arg pro
 122/41
 GCT CGC CTT TTT TTC ATC AAC GTT GGA CTG CCG CAG TGG CGA TGT TGG TCG CCG GCG TGT
 ala arg leu phe phe ile asn val gly leu pro gln trp arg cys trp ser pro ala cys
 182/61
 TCG GTC ACC TGA CGG TCG GGA TGT TCC TTG GGT CTC GGG TTG CTG CTG GGT TTG CTC AAT
 ser val thr OPA arg ser gly cys ser leu gly leu gly leu leu leu gly leu leu asn
 242/81
 GCC CTG CTG GTG CGG CGT TCG GCC GAG TCG ATC ACC GCC AAA GAG CAC CCG TTA AAA CCG
 ala leu leu val arg arg ser ala glu ser ile thr ala lys glu his pro leu lys arg
 302/101
 TCG ATG GCC CTC AAC TCG GCA TCG CGA CTG GCG ATT ATC ACC ATG CCT CGG GCT GAT C
 ser met ala leu asn ser ala ser arg leu ala ile ile thr met pro arg ala asp

SEQ ID No.17B

FIGURE 17B

33/11
 GGG CCA CCG ATC AGT CGA TCG GGT GGT TTC CGC TCC ATC AGC CCG GAA TTG AGG TGC CGC
 gly pro pro ile ser arg ser gly gly phe arg ser ile ser pro glu leu arg cys arg
 63/21
 AGT GAC GAC ACC AGC GCA GGA CGC GCC GTT GGT GTT TCC CTC TGT TGC TTT CCC GTC CGG
 ser asp asp thr ser ala gly arg ala val gly val ser leu cys cys phe pro val arg
 123/41
 CTC GCC TTT TTT TCA TCA ACG TTG GAC TGC CGC AGT GGC GAT GTT GGT CGC CGG CGT GTT
 leu ala phe phe ser ser thr leu asp cys arg ser gly asp val gly arg arg arg val
 183/61
 CGG TCA CCT GAC GGT CGG GAT GTT CCT TGG GTC TCG GGT TGC TGC TGG GTT TGC TCA ATG
 arg ser pro asp gly arg asp val pro trp val ser gly cys cys trp val cys ser met
 243/81
 CCC TGC TGG TGC GGC GTT CGG CCG AGT CGA TCA CCG CCA AAG AGC ACC CGT TAA AAC GGT
 pro cys trp cys gly val arg pro ser arg ser pro pro lys ser thr arg OCH asn gly
 303/101
 CGA TGG CCC TCA ACT CGG CAT CGC GAC TGG CGA TTA TCA CCA TGC CTC GGG CTG ATC
 arg trp pro ser thr arg his arg asp trp arg leu ser pro cys leu gly leu ile

SEQ ID No.17C

FIGURE 17C

part of the nucleotide sequence of seq17A

1/1
 ggc tag aac ccc gaa gga gac ctc gcg ggt tgc cgg ccc ccg gcc cat cgg atg cgt atc
 gly AMB asn pro glu gly asp leu ala gly cys arg pro pro ala his arg met arg ile
 61/21
 cgg tcg cgc cga ttc acg acc gac ata ggg agc tac ccc ttg ggt gat tcc ggt gcg acg
 arg ser arg arg phe thr thr asp ile gly ser tyr pro leu gly asp ser gly ala thr
 121/41
 act gcg ata cgc tcg gcg ggc cac cga tca gtc gat cgg gtg gtt tcc gct cca tca gcc
 thr ala ile arg ser ala gly his arg ser val asp arg val val ser ala pro ser ala
 181/61
 cgg aat tga ggt gcc gca gtg acg aca cca gcg cag gac gcg ccg ttg gtg ttt ccc tct
 arg asn OPA gly ala ala val thr thr pro ala gln asp ala pro leu val phe pro ser
 241/81
 gtt gct ttc cgt ccg gtt cgc ctt ttt ttc atc aac gtt gga ctg gcc gca gtg gcg atg
 val ala phe arg pro val arg leu phe phe ile asn val gly leu ala ala val ala met
 301/101
 ttg gtc gcc ggc gtg ttc ggt cac ctg acg gtc ggg atg ttc ttg ggt ctc ggg ttg ctg
 leu val ala gly val phe gly his leu thr val gly met phe leu gly leu gly leu leu
 361/121
 ctg ggt ttg ctc aat gcc ctg ctg gtg cgg cgt tcg gcc gag tcg atc acc gcc aaa gag
 leu gly leu leu asn ala leu leu val arg arg ser ala glu ser ile thr ala lys glu
 421/141
 cac ccg tta aaa cgg tcg atg gcc ctc aac tcg gca tcg cga ctg gcg att atc acc atc
 his pro leu lys arg ser met ala leu asn ser ala ser arg leu ala ile ile thr ile
 481/161
 ctc ggg ctg atc
 leu gly leu ile

SEQ ID No.17A'

FIGURE 17A'

1/1 31/11
gct aga acc ccg aag gag acc tcg cgg gtt gcc ggc ccc cgg ccc atc gga tgc gta tcc
ala arg thr pro lys glu thr ser arg val ala gly pro arg pro ile gly cys val ser
61/21 91/31
ggt cgc gcc gat tca cga ccg aca tag gga gct acc cct tgg gtg att ccg gtg cga cga
gly arg ala asp ser arg pro thr AMB gly ala thr pro trp val ile pro val arg arg
121/41 151/51
ctg cga tac gct cgg cgg gcc acc gat cag tcg atc ggg tgg ttt ccg ctc cat cag ccc
leu arg tyr ala arg arg ala thr asp gln ser ile gly trp phe pro leu his gln pro
181/61 211/71
gga att gag gtg ccg cag tga cga cac cag cgc agg acg cgc cgt tgg tgt ttc cct ctg
gly ile glu val pro gln OPA arg his gln arg arg thr arg arg trp cys phe pro leu
241/81 271/91
ttg ctt tcc gtc cgg ttc gcc ttt ttt tca tca acg ttg gac tgg ccg cag tgg cga tgt
leu leu ser val arg phe ala phe phe ser ser thr leu asp trp pro gln trp arg cys
301/101 331/111
tgg tcg ccg gcg tgt tcg gtc acc tga cgg tcg gga tgt tct tgg gtc tcg ggt tgc tgc
trp ser pro ala cys ser val thr OPA arg ser gly cys ser trp val ser gly cys cys
361/121 391/131
tgg gtt tgc tca atg ccc tgc tgg tgc gcc gtt cgg ccg agt cga tca ccg cca aag agc
trp val cys ser met pro cys trp cys gly val arg pro ser arg ser pro pro lys ser
421/141 451/151
acc cgt taa aac ggt cga tgg ccc tca act cgg cat cgc gac tgg cga tta tca cca tcc
thr arg OCH asn gly arg trp pro ser thr arg his arg asp trp arg leu ser pro ser
481/161
tcg ggc tga tc
ser gly OPA

SEQ ID No.17B'

FIGURE 17B'

1/1 31/11
cta gaa ccc cga agg aga cct cgc ggg ttg ccg gcc ccc ggc cca tcg gat gcg tat ccg
leu glu pro arg arg arg pro arg gly leu pro ala pro gly pro ser asp ala tyr pro
61/21 91/31
gtc gcg ccg att cac gac cga cat agg gag cta ccc ctt ggg tga ttc cgg tgc gac gac
val ala pro ile his asp arg his arg glu leu pro leu gly OPA phe arg cys asp asp
121/41 151/51
tgc gat acg ctc ggc ggg cca ccg atc agt cga tcg ggt ggt ttc cgc tcc atc agc ccg
cys asp thr leu gly gly pro pro ile ser arg ser gly gly phe arg ser ile ser pro
181/61 211/71
gaa ttg agg tgc cgc agt gac gac acc agc gca gga cgc gcc gtt ggt gtt tcc ctc tgt
glu leu arg cys arg ser asp asp thr ser ala gly arg ala val gly val ser leu cys
241/81 271/91
tgc ttt ccg tcc ggt tcg cct ttt ttt cat caa cgt tgg act ggc cgc agt ggc gat gtt
cys phe pro ser gly ser pro phe phe his gln arg trp thr gly arg ser gly asp val
301/101 331/111
ggt cgc ccg cgt gtt cgg tca cct gac ggt cgg gat gtt ctt ggg tct ccg gtt gct gct
gly arg arg arg val arg ser pro asp gly arg asp val leu gly ser arg val ala ala
361/121 391/131
ggg ttt gct caa tgc cct gct ggt gcg gcg ttc ggc cga gtc gat cac cgc caa aga gca
gly phe ala gln cys pro ala gly ala ala phe gly arg val asp his arg gln arg ala
421/141 451/151
ccc gtt aaa acg gtc gat ggc cct caa ctc ggc atc gcg act ggc gat tat cac cat cct
pro val lys thr val asp gly pro gln leu gly ile ala thr gly asp tyr his his pro
481/161
cgg gct gat c
arg ala asp

SEQ ID No.17C'

FIGURE 17C'

61/185

sequence Rv1303 predicted by Cole et al. (Nature 393:537-544) and partially containing Seq17A'

```

1/1
atg acg aca cca gcg cag gac gcg ccg ttg gtg ttt ccc tct gtt gct ttc cgt ccg gtt
met thr thr pro ala gln asp ala pro leu val phe pro ser val ala phe arg pro val
61/21
cgc ctt ttt ttc atc aac gtt gga ctg gcc gca gtg gcg atg ttg gtc gcc gcc gtg ttc
arg leu phe phe ile asn val gly leu ala ala val ala met leu val ala gly val phe
121/41
ggt cac ctg acg gtc ggg atg ttc ttg ggt ctc ggg ttg ctg ctg ggt ttg ctc aat gcc
gly his leu thr val gly met phe leu gly leu gly leu leu leu gly leu leu asn ala
181/61
ctg ctg gtg cgg cgt tgc gcc gag tgc atc acc gcc aaa gag cac ccg tta aaa cgg tgc
leu leu val arg arg ser ala glu ser ile thr ala lys glu his pro leu lys arg ser
241/81
atg gcc ctc aac tgc gca tgc cga ctg gcg att atc acc atc ctc ggg ctg atc atc gcc
met ala leu asn ser ala ser arg leu ala ile ile thr ile leu gly leu ile ile ala
301/101
tac att ttc cgg ccc gct gga ttg ggc gtc gtg ttc ggg ctg gca ttc ttc cag gtg ctg
tyr ile phe arg pro ala gly leu gly val val phe gly leu ala phe phe gln val leu
361/121
ctg gtg gca acg acg gcc ctg ccg gtc ctg aag aag ctg cgc act gcg acc gag gaa ccg
leu val ala thr thr ala leu pro val leu lys lys leu arg thr ala thr glu glu pro
421/141
gtc gca act tat tct tcc aat ggc cag acc ggg gga tgc gaa gga agg agc gcc agc gat
val ala thr tyr ser ser asn gly gln thr gly gly ser glu gly arg ser ala ser asp
481/161
gac tga
asp OPA

```

SEQ ID No.17D

FIGURE 17D

Orf according to Cole et al. (Nature 393:537-544) and containing Rv1303

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1/1
tga ggt gcc gca gtg acg aca cca gcg cag gac gcg ccg ttg gtg ttt ccc tct gtt gct
OPA gly ala ala val thr thr pro ala gln asp ala pro leu val phe pro ser val ala
61/21
ttc cgt ccg gtt cgc ctt ttt ttc atc aac gtt gga ctg gcc gca gtg gcg atg ttg gtc
phe arg pro val arg leu phe phe ile asn val gly leu ala ala val ala met leu val
121/41
gcc gcc gtg ttc ggt cac ctg acg gtc ggg atg ttc ttg ggt ctc ggg ttg ctg ctg ggt
ala gly val phe gly his leu thr val gly met phe leu gly leu gly leu leu leu gly
181/61
ttg ctc aat gcc ctg ctg gtg cgg cgt tgc gcc gag tgc atc acc gcc aaa gag cac ccg
leu leu asn ala leu leu val arg arg ser ala glu ser ile thr ala lys glu his pro
241/81
tta aaa cgg tgc atg gcc ctc aac tgc gca tgc cga ctg gcg att atc acc atc ctc ggg
leu lys arg ser met ala leu asn ser ala ser arg leu ala ile ile thr ile leu gly
301/101
ctg atc atc gcc tac att ttc cgg ccc gct gga ttg ggc gtc gtg ttc ggg ctg gca ttc
leu ile ile ala tyr ile phe arg pro ala gly leu gly val val phe gly leu ala phe
361/121
ttc cag gtg ctg ctg gtg gca acg acg gcc ctg ccg gtc ctg aag aag ctg cgc act gcg
phe gln val leu leu val ala thr thr ala leu pro val leu lys lys leu arg thr ala
421/141
acc gag gaa ccg gtc gca act tat tct tcc aat ggc cag acc ggg gga tgc gaa gga agg
thr glu glu pro val ala thr tyr ser ser asn gly gln thr gly gly ser glu gly arg
481/161
agc gcc agc gat gac tga
ser ala ser asp asp OPA

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SEQ ID No.17F

FIGURE 17F

62/185

31/11
 GTC GAA CAG GTA CGG AAG GCG CCG TCG GTC GCT CGG TCC GCT GGT ATC TCG TGT TCA GCC
 val glu gln val arg lys ala pro ser val ala arg ser ala gly ile ser cys ser ala
 61/21
 AGC CAG CGG CCG TTA ACG TGG CCG AAC AGG TCG TCT TGG GGT CGG GCA TCA GCG TCG ATG
 ser gln arg pro leu thr trp pro asn arg ser ser trp gly arg ala ser ala ser met
 121/41
 TGG CTC AGG TCG ATA CCC GAG GGG ATG GCA AGT GTC ACC CCG CCA TCC TTC CAC CTC TTT
 trp leu arg ser ile pro glu gly met ala ser val thr pro pro ser phe his leu phe
 181/61
 TCG GGT GCA ACG ATC GGG CCA TGC CTG ACG GGG AGC AGA GCC AGC CAC CGG CCC AAG AAG
 ser gly ala thr ile gly pro cys leu thr gly ser arg ala ser his arg pro lys lys
 241/81
 ATG CGG AAG ACG ACT CGC GGC CCG ACG CCG CGG AGG CCG CCG CGG CCG AAC CCA AAT CAT
 met arg lys thr thr arg gly pro thr pro arg arg pro pro arg pro asn pro asn his
 301/101
 CAG CCG GTC CCG ATG TTC TCG ACC TAC GGT ATC GCC TCG ACA CTA CTC GGC GTG CTA TCG
 gln pro val pro met phe ser thr tyr gly ile ala ser thr leu leu gly val leu ser
 361/121
 GTC GCC GCG GTC GTG CTG GGT GCG ATG ATC
 val ala ala val val leu gly ala met ile

SEQ ID No.18A

FIGURE 18A

32/11
 TCG AAC AGG TAC GGA AGG CGC CGT CGG TCG CTC GGT CCG CTG GTA TCT CGT GTT CAG CCA
 ser asn arg tyr gly arg arg arg arg ser leu gly pro leu val ser arg val gln pro
 62/21
 GCC AGC GGC CGT TAA CGT GGC CGA ACA GGT CGT CTT GGG GTC GGG CAT CAG CGT CGA TGT
 ala ser gly arg OCH arg gly arg thr gly arg leu gly val gly his gln arg arg cys
 122/41
 GGC TCA GGT CGA TAC CCG AGG GGA TGG CAA GTG TCA CCC CGC CAT CCT TCC ACC TCT TTT
 gly ser gly arg tyr pro arg gly trp gln val ser pro arg his pro ser thr ser phe
 182/61
 CGG GTG CAA CGA TCG GGC CAT GCC TGA CGG GGA GCA GAG CCA GCC ACC GGC CCA AGA AGA
 arg val gln arg ser gly his ala OPA arg gly ala glu pro ala thr gly pro arg arg
 242/81
 TGC GGA AGA CGA CTC GCG GCC CGA CGC CGC GGA GGC CGC CGC GGC CGA ACC CAA ATC ATC
 cys gly arg arg leu ala ala arg arg arg gly gly arg arg gly arg thr gln ile ile
 302/101
 AGC CGG TCC CGA TGT TCT CGA CCT ACG GTA TCG CCT CGA CAC TAC TCG GCG TGC TAT CGG
 ser arg ser arg cys ser arg pro thr val ser pro arg his tyr ser ala cys tyr arg
 362/121
 TCG CCG CGG TCG TGC TGG GTG CGA TGA TC
 ser pro arg ser cys trp val arg OPA

SEQ ID No.18B

FIGURE 18B

63/185

3/1
CGA ACA GGT ACG GAA GGC GCC GTC GGT CGC TCG GTC CGC TGG TAT CTC GTG TTC AGC CAG
arg thr gly thr glu gly ala val gly arg ser val arg trp tyr leu val phe ser gln
63/21
CCA GCG GCC GTT AAC GTG GCC GAA CAG GTC GTC TTG GGG TCG GGC ATC AGC GTC GAT GTG
pro ala ala val asn val ala glu gln val val leu gly ser gly ile ser val asp val
123/41
GCT CAG GTC GAT ACC CGA GGG GAT GGC AAG TGT CAC CCC GCC ATC CTT CCA CCT CTT TTC
ala gln val asp thr arg gly asp gly lys cys his pro ala ile leu pro pro leu phe
183/61
GGG TGC AAC GAT CGG GCC ATG CCT GAC GGG GAG CAG AGC CAG CCA CCG GCC CAA GAA GAT
gly cys asn asp arg ala met pro asp gly glu gln ser gln pro pro ala gln glu asp
243/81
GCG GAA GAC GAC TCG CGG CCC GAC GCC GCG GAG GCC GCC GCG GCC GAA CCC AAA TCA TCA
ala glu asp asp ser arg pro asp ala ala glu ala ala ala glu pro lys ser ser
303/101
GCC GGT CCC GAT GTT CTC GAC CTA CGG TAT CGC CTC GAC ACT ACT CGG CGT GCT ATC GGT
ala gly pro asp val leu asp leu arg tyr arg leu asp thr thr arg arg ala ile gly
363/121
CGC CGC GGT CGT GCT GGG TGC GAT GAT C
arg arg gly arg ala gly cys asp asp

SEQ ID No.18C

FIGURE 18C

part of the nucleotide sequence of seq18A

1/1
GAA GGC GCC GTC GGT CGC TCG GTC CGC TGG TAT CTC GTG TTC AGC CAG CCA GCG GCC GTT
glu gly ala val gly arg ser val arg trp tyr leu val phe ser gln pro ala ala val
61/21
AAC GTG GCC GAA CAG GTC GTC TTG GGG TCG GGC ATC AGC GTC GAT GTG GCT CAG GTC GAT
asn val ala glu gln val val leu gly ser gly ile ser val asp val ala gln val asp
121/41
ACC CGA GGG GAT GGC AAG TGT CAC CCC GCC ATC CTT CCA CCT CTT TTC GGG TGC AAC GAT
thr arg gly asp gly lys cys his pro ala ile leu pro pro leu phe gly cys asn asp
181/61
CGG GCC ATG CCT GAC GGG GAG CAG AGC CAG CCA CCG GCC CAA GAA GAT GCG GAA GAC GAC
arg ala met pro asp gly glu gln ser gln pro pro ala gln glu asp ala glu asp asp
241/81
TCG CGG CCC GAC GCC GCG GAG GCC GCC GCG GCC GAA CCC AAA TCA TCA GCC GGT CCG ATG
ser arg pro asp ala ala glu ala ala ala ala glu pro lys ser ser ala gly pro met
301/101
TTC TCG ACC TAC GGT ATC GCC TCG ACA CTA CTC GGC GTG CTA TCG GTC GCC GCG GTC GTG
phe ser thr tyr gly ile ala ser thr leu leu gly val leu ser val ala ala val val
361/121
CTG GGT GCG ATG ATC
leu gly ala met ile

SEQ ID No.18A'

FIGURE 18A'

64/185

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1/1                               31/11
CGG AAG GCG CCG TCG GTC GCT CGG TCC GCT GGT ATC TCG TGT TCA GCC AGC CAG CGG CCG
arg lys ala pro ser val ala arg ser ala gly ile ser cys ser ala ser gln arg pro
61/21                               91/31
TTA ACG TGG CCG AAC AGG TCG TCT TGG GGT CGG GCA TCA GCG TCG ATG TGG CTC AGG TCG
leu thr trp pro asn arg ser ser trp gly arg ala ser ala ser met trp leu arg ser
121/41                               151/51
ATA CCC GAG GGG ATG GCA AGT GTC ACC CCG CCA TCC TTC CAC CTC TTT TCG GGT GCA ACG
ile pro glu gly met ala ser val thr pro pro ser phe his leu phe ser gly ala thr
181/61                               211/71
ATC GGG CCA TGC CTG ACG GGG AGC AGA GCC AGC CAC CGG CCC AAG AAG ATG CGG AAG ACG
ile gly pro cys leu thr gly ser arg ala ser his arg pro lys lys met arg lys thr
241/81                               271/91
ACT CGC GGC CCG ACG CCG CGG AGG CCG CCG CGG CCG AAC CCA AAT CAT CAG CCG GTC CGA
thr arg gly pro thr pro arg arg pro pro arg pro asn pro asn his gln pro val arg
301/101                               331/111
TGT TCT CGA CCT ACG GTA TCG CCT CGA CAC TAC TCG GCG TGC TAT CGG TCG CCG CGG TCG
cys ser arg pro thr val ser pro arg his tyr ser ala cys tyr arg ser pro arg ser
361/121
TGC TGG GTG CGA TGA TC
cys trp val arg OPA

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SEQ ID No.18B'

FIGURE 18B'

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1/1                               31/11
GGA AGG CGC CGT CGG TCG CTC GGT CCG CTG GTA TCT CGT GTT CAG CCA GCC AGC GGC CGT
gly arg arg arg arg ser leu gly pro leu val ser arg val gln pro ala ser gly arg
61/21                               91/31
TAA CGT GGC CGA ACA GGT CGT CTT GGG GTC GGG CAT CAG CGT CGA TGT GGC TCA GGT CGA
OCH arg gly arg thr gly arg leu gly val gly his gln arg arg cys gly ser gly arg
121/41                               151/51
TAC CCG AGG GGA TGG CAA GTG TCA CCC CGC CAT CCT TCC ACC TCT TTT CGG GTG CAA CGA
tyr pro arg gly trp gln val ser pro arg his pro ser thr ser phe arg val gln arg
181/61                               211/71
TCG GGC CAT GCC TGA CGG GGA GCA GAG CCA GCC ACC GGC CCA AGA AGA TGC GGA AGA CGA
ser gly his ala OPA arg gly ala glu pro ala thr gly pro arg arg cys gly arg arg
241/81                               271/91
CTC GCG GCC CGA CGC CGC GGA GGC CGC CGC GGC CGA ACC CAA ATC ATC AGC CGG TCC GAT
leu ala ala arg arg arg gly gly arg arg gly arg thr gln ile ile ser arg ser asp
301/101                               331/111
GTT CTC GAC CTA CGG TAT CGC CTC GAC ACT ACT CGG CGT GCT ATC GGT CGC CGC GGT CGT
val leu asp leu arg tyr arg leu asp thr thr arg arg ala ile gly arg arg gly arg
361/121
GCT GGG TGC GAT GAT C
ala gly cys asp asp

```

SEQ ID No.18C'

FIGURE 18C'

sequence Rv0199 predicted by Cole et al. (Nature 393:537-544) and containing seq18A'

1/1	31/11
atg cct gac ggg gag cag agc cag cca ccg	gcc caa gaa gat gcg gaa gac gac tcg cgg
Met pro asp gly glu gln ser gln pro pro	ala gln glu asp ala glu asp asp ser arg
61/21	91/31
ccc gac gcc gcg gag gcc gcc gcg gcc gaa	ccc aaa tca tca gcc ggt ccg atg ttc tcg
pro asp ala ala glu ala ala ala ala glu	pro lys ser ser ala gly pro met phe ser
121/41	151/51
acc tac ggt atc gcc tcg aca cta ctc ggc	gtg cta tcg gtc gcc gcg gtc gtg ctg ggt
thr tyr gly ile ala ser thr leu leu gly	val leu ser val ala ala val val leu gly
181/61	211/71
gcg atg atc tgg tcc gca cac cgc gat gac	tcc gcc gag cgt acc tac ctg acc cgg gtc
ala met ile trp ser ala his arg asp asp	ser gly glu arg thr tyr leu thr arg val
241/81	271/91
atg ctg acc gcc gct gaa tgg acg gcc gtg	ctg atc aac atg aac gcc gac aac atc gat
met leu thr ala ala glu trp thr ala val	leu ile asn met asn ala asp asn ile asp
301/101	331/111
gcc agc ctg cag cga ctg cac gac gga acg	gtc ggt caa ctc aac acc gac ttc gac gct
ala ser leu gln arg leu his asp gly thr	val gly gln leu asn thr asp phe asp ala
361/121	391/131
gtc gtg cag ccc tac cgg cag gtg gtg gag	aag ttg cgg acg cac agc agc ggc agg atc
val val gln pro tyr arg gln val val glu	lys leu arg thr his ser ser gly arg ile
421/141	451/151
gag gcg gta gcg atc gat acg gtg cac cgc	gag ctg gat acc cag tcc ggt gcc gcc cga
glu ala val ala ile asp thr val his arg	glu leu asp thr gln ser gly ala ala arg
481/161	511/171
ccg gta gta acc acg aaa ttg cca ccg ttt	gcc act cgc acc gac tcg gtg ctg ctg gtc
pro val val thr thr lys leu pro pro phe	ala thr arg thr asp ser val leu leu val
541/181	571/191
gcg acg tcg gtc agt gag aac gcc ggc gcc	aaa ccc cag acc gtg cac tgg aac ttg cgg
ala thr ser val ser glu asn ala gly ala	lys pro gln thr val his trp asn leu arg
601/201	631/211
ctc gat gtc tcc gat gtg gac ggc aag ctg	atg atc tcc cgg ttg gag tcg att cga tga
leu asp val ser asp val asp gly lys leu	met ile ser arg leu glu ser ile arg OPA

SEQ ID No.18D

FIGURE 18D

ORF according to Cole et al. (Nature 393:537-544) and containing Rv0199

1/1	taa tcc gat gcc gga ttg ggt gaa atg cac	31/11	caa gta acg ggt cga gtc ttt gga atc ggt
OCH ser asp ala gly leu gly glu met his	gln val thr gly arg val phe gly ile gly	91/31	gln val thr gly arg val phe gly ile gly
61/21	atc gac ata gac tcc gat gcc gcc gcc cac	151/51	gln val thr gly arg val phe gly ile gly
ile asp ile asp ser asp ala ala ala his	ala gly thr leu gln ser ala lys gly gly	211/71	gln val thr gly arg val phe gly ile gly
121/41	ggc caa ttc ggt ggc gtc ggc cgc gct gtc	271/91	gln val thr gly arg val phe gly ile gly
gly gln phe gly gly val gly arg ala val	asn arg gly gln phe val val gln arg leu	331/111	gln val thr gly arg val phe gly ile gly
181/61	cac ccc tgc gcg ctc gac ggc ttc ctc gtc	391/131	gln val thr gly arg val phe gly ile gly
his pro cys ala leu asp gly phe leu val	gag gaa gct ggc gta gag gtc gcc gat gcg	451/151	gln val thr gly arg val phe gly ile gly
241/81	ctg cgc atc ggt gcc tac cgc agc acc tgc	511/171	gln val thr gly arg val phe gly ile gly
leu arg ile gly ala tyr arg ser thr cys	gln val thr gly arg val phe gly ile gly	571/191	gln val thr gly arg val phe gly ile gly
301/101	ttg tgt ctc ggc gcg gtc gaa cag gct acg	631/211	gln val thr gly arg val phe gly ile gly
leu cys leu gly ala val glu gln ala thr	gln val thr gly arg val phe gly ile gly	691/231	gln val thr gly arg val phe gly ile gly
361/121	tat ctc gtg ttc agc cag cca gcg gcc gtt	751/251	gln val thr gly arg val phe gly ile gly
tyr leu val phe ser gln pro ala ala val	asn val ala glu gln val val leu gly ser	811/271	gln val thr gly arg val phe gly ile gly
421/141	ggc atc agc gtc gat gtg gct cag gtc gat	871/291	gln val thr gly arg val phe gly ile gly
gly ile ser val asp val ala gln val asp	thr arg gly asp gly lys cys his pro ala	931/311	gln val thr gly arg val phe gly ile gly
481/161	atc ctt cca cct ctt ttc ggg tgc aac gat	991/331	gln val thr gly arg val phe gly ile gly
ile leu pro pro leu phe gly cys asn asp	cgg gcc atg cct gac ggg gag cag agc cag	1051/351	gln val thr gly arg val phe gly ile gly
541/181	cca ccg gcc caa gaa gat gcg gaa gac gac	1111/371	gln val thr gly arg val phe gly ile gly
pro pro ala gln glu asp ala glu asp asp	ser arg pro asp ala ala glu ala ala ala	1171/391	gln val thr gly arg val phe gly ile gly
601/201	gcc gaa ccc aaa tca tca gcc ggt ccg atg	1231/411	gln val thr gly arg val phe gly ile gly
ala glu pro lys ser ser ala gly pro met	phe ser thr tyr gly ile ala ser thr leu	1291/431	gln val thr gly arg val phe gly ile gly
661/221	ctc ggc gtg cta tcg gtc gcc gcg gtc gtg	1351/451	gln val thr gly arg val phe gly ile gly
leu gly val leu ser val ala ala val val	leu gly ala met ile trp ser ala his arg	1411/471	gln val thr gly arg val phe gly ile gly
721/241	gat gac tcc ggc gag cgt acc tac ctg acc	1471/491	gln val thr gly arg val phe gly ile gly
asp asp ser gly glu arg thr tyr leu thr	arg val met leu thr ala ala glu trp thr	1531/511	gln val thr gly arg val phe gly ile gly
781/261	gcc gtg ctg atc aac atg aac gcc gac aac	1591/531	gln val thr gly arg val phe gly ile gly
ala val leu ile asn met asn ala asp asn	ile asp ala ser leu gln arg leu his asp	1651/551	gln val thr gly arg val phe gly ile gly
841/281	gga acg gtc ggt caa ctc aac acc gac ttc	1711/571	gln val thr gly arg val phe gly ile gly
gly thr val gly gln leu asn thr asp phe	asp ala val val gln pro tyr arg gln val	1771/591	gln val thr gly arg val phe gly ile gly
901/301	gtg gag aag ttg cgg acg cac agc agc ggc	1831/611	gln val thr gly arg val phe gly ile gly
val glu lys leu arg thr his ser ser gly	agg atc gag gcg gta gcg atc gat acg gtg	1891/631	gln val thr gly arg val phe gly ile gly
961/321	cac cgc gag ctg gat acc cag tcc ggt gcc	1951/651	gln val thr gly arg val phe gly ile gly
his arg glu leu asp thr gln ser gly ala	ala arg pro val val thr thr lys leu pro	2011/671	gln val thr gly arg val phe gly ile gly
1021/341	ccg ttt gcc act cgc acc gac tcg gtg ctg	2071/691	gln val thr gly arg val phe gly ile gly
pro phe ala thr arg thr asp ser val leu	leu val ala thr ser val ser glu asn ala	2131/711	gln val thr gly arg val phe gly ile gly
1081/361	ggc gcc aaa ccc cag acc gtg cac tgg aac	2191/731	gln val thr gly arg val phe gly ile gly
gly ala lys pro gln thr val his trp asn	leu arg leu asp val ser asp val asp gly	2251/751	gln val thr gly arg val phe gly ile gly
1141/381	aag ctg atg atc tcc cgg ttg gag tcg att	2311/771	gln val thr gly arg val phe gly ile gly
lys leu met ile ser arg leu glu ser ile	arg opa		

SEQ ID No.18F

FIGURE 18F

31/11
 GTT GCG CAA CGG GGT GAG CAC CGA CGC GAT GAT GGC GCA ACT ATC GAA ACT GCA GGA CAT
 val ala gln arg gly glu his arg arg asp asp gly ala thr ile glu thr ala gly his
 61/21 91/31
 CGC CAA CGC CAA CGA CGG CAC TCG CGC GGT GGG CAC CCC TGG CTA TCA GGC CAG CGT CGA
 arg gln arg gln arg arg his ser arg gly gly his pro trp leu ser gly gln arg arg
 121/41 151/51
 CTA TGT GGT AAA CAC ACT GCG CAA CAG CGG TTT TGA TGT GCA AAC CCC GGA GTT CTC CGC
 leu cys gly lys his thr ala gln gln arg phe OPA cys ala asn pro gly val leu arg
 181/61 211/71
 TCG CGT GTT CAA GGC CGA AAA AGG GGT GGT GAC CCT CGG CGG CAA CAC CGT GGA GGC GAG
 ser arg val gln gly arg lys arg gly gly asp pro arg arg gln his arg gly gly glu
 241/81 271/91
 GGC GCT CGA GTA CAG CCT CGG CAC ACC GCC GGA CGG GGT GAC GGG CCC GCT GGT GGC TGC
 gly ala arg val gln pro arg his thr ala gly arg gly asp gly pro ala gly gly cys
 301/101 331/111
 CCC CGC CGA CGA CAG TCC GGG CTG CAG TCC GTC GGA CTA CGA CAG GCT GCC GGT GTC CGG
 pro arg arg arg gln ser gly leu gln ser val gly leu arg gln ala ala gly val arg
 361/121
 TGC GGT GGT GCT GGT AGA TC
 cys gly gly ala gly arg

SEQ ID No.19A

FIGURE 19A

32/11
 TTG CGC AAC GGG GTG AGC ACC GAC GCG ATG ATG GCG CAA CTA TCG AAA CTG CAG GAC ATC
 leu arg asn gly val ser thr asp ala met met ala gln leu ser lys leu gln asp ile
 62/21 92/31
 GCC AAC GCC AAC GAC GGC ACT CGC GCG GTG GGC ACC CCT GGC TAT CAG GCC AGC GTC GAC
 ala asn ala asn asp gly thr arg ala val gly thr pro gly tyr gln ala ser val asp
 122/41 152/51
 TAT GTG GTA AAC ACA CTG CGC AAC AGC GGT TTT GAT GTG CAA ACC CCG GAG TTC TCC GCT
 tyr val val asn thr leu arg asn ser gly phe asp val gln thr pro glu phe ser ala
 182/61 212/71
 CGC GTG TTC AAG GCC GAA AAA GGG GTG GTG ACC CTC GGC GGC AAC ACC GTG GAG GCG AGG
 arg val phe lys ala glu lys gly val val thr leu gly gly asn thr val glu ala arg
 242/81 272/91
 GCG CTC GAG TAC AGC CTC GGC ACA CCG CCG GAC GGG GTG ACG GGC CCG CTG GTG GCT GCC
 ala leu glu tyr ser leu gly thr pro pro asp gly val thr gly pro leu val ala ala
 302/101 332/111
 CCC GCC GAC GAC AGT CCG GGC TGC AGT CCG TCG GAC TAC GAC AGG CTG CCG GTG TCC GGT
 pro ala asp asp ser pro gly cys ser pro ser asp tyr asp arg leu pro val ser gly
 362/121
 GCG GTG GTG CTG GTA GAT C
 ala val val leu val asp

SEQ ID No.19B

FIGURE 19B

33/11
 TGC GCA ACG GGG TGA GCA CCG ACG CGA TGA TGG CGC AAC TAT CGA AAC TGC AGG ACA TCG
 cys ala thr gly OPA ala pro thr arg OPA trp arg asn tyr arg asn cys arg thr ser
 63/21
 CCA ACG CCA ACG ACG GCA CTC GCG CGG TGG GCA CCC CTG GCT ATC AGG CCA GCG TCG ACT
 pro thr pro thr thr ala leu ala arg trp ala pro leu ala ile arg pro ala ser thr
 123/41
 ATG TGG TAA ACA CAC TGC GCA ACA GCG GTT TTG ATG TGC AAA CCC CGG AGT TCT CCG CTC
 met trp OCH thr his cys ala thr ala val leu met cys lys pro arg ser ser pro leu
 183/61
 GCG TGT TCA AGG CCG AAA AAG GGG TGG TGA CCC TCG GCG GCA ACA CCG TGG AGG CGA GGG
 ala cys ser arg pro lys lys gly trp OPA pro ser ala ala thr pro trp arg arg gly
 243/81
 CGC TCG AGT ACA GCC TCG GCA CAC CGC CGG ACG GGG TGA CGG GCC CGC TGG TGG CTG CCC
 arg ser ser thr ala ser ala his arg arg thr gly OPA arg ala arg trp trp leu pro
 303/101
 CCG CCG ACG ACA GTC CGG GCT GCA GTC CGT CGG ACT ACG ACA GGC TGC CGG TGT CCG GTG
 pro pro thr thr val arg ala ala val arg arg thr thr thr gly cys arg cys pro val
 363/121
 CGG TGG TGC TGG TAG ATC
 arg trp cys trp AMB ile

SEQ ID No.19C

FIGURE 19C

part of the nucleotide sequence of seq19A

1/1
 CTA TCG AAA CTG CAG GAC ATC GCC AAC GCC AAC GAC GGC ACT CGC GCG GTG GGC ACC CCT
 leu ser lys leu gln asp ile ala asn ala asn asp gly thr arg ala val gly thr pro
 61/21
 GGC TAT CAG GCC AGC GTC GAC TAT GTG GTA AAC ACA CTG CGC AAC AGC GGT TTT GAT GTG
 gly tyr gln ala ser val asp tyr val val asn thr leu arg asn ser gly phe asp val
 121/41
 CAA ACC CCG GAG TTC TCC GCT CGC GTG TTC AAG GCC GAA AAA GGG GTG GTG ACC CTC GGC
 gln thr pro glu phe ser ala arg val phe lys ala glu lys gly val val thr leu gly
 181/61
 GGC AAC ACC GTG GAG GCG AGG GCG CTC GAG TAC AGC CTC GGC ACA CCG CCG GAC GGG GTG
 gly asn thr val glu ala arg ala leu glu tyr ser leu gly thr pro pro asp gly val
 241/81
 ACG GGC CCG CTG GTG GCT GCC CCC GCC GAC GAC AGT CCG GGC TGC AGT CCG TCG GAC TAC
 thr gly pro leu val ala ala pro ala asp asp ser pro gly cys ser pro ser asp tyr
 301/101
 GAC AGG CTG CCG GTG TCC GGT GCG GTG GTG CTG GTA GAT C
 asp arg leu pro val ser gly ala val val leu val asp

SEQ ID No.19A'

FIGURE 19A

1/1 31/11
TAT CGA AAC TGC AGG ACA TCG CCA ACG CCA ACG ACG GCA CTC GCG CGG TGG GCA CCC CTG
tyr arg asn cys arg thr ser pro thr pro thr thr ala leu ala arg trp ala pro leu
61/21 91/31
GCT ATC AGG CCA GCG TCG ACT ATG TGG TAA ACA CAC TGC GCA ACA GCG GTT TTG ATG TGC
ala ile arg pro ala ser thr met trp OCH thr his cys ala thr ala val leu met cys
121/41 151/51
AAA CCC CGG AGT TCT CCG CTC GCG TGT TCA AGG CCG AAA AAG GGG TGG TGA CCC TCG GCG
lys pro arg ser ser pro leu ala cys ser arg pro lys lys gly trp OPA pro ser ala
181/61 211/71
GCA ACA CCG TGG AGG CGA GGG CGC TCG AGT ACA GCC TCG GCA CAC CGC CGG ACG GGG TGA
ala thr pro trp arg arg gly arg ser ser thr ala ser ala his arg arg thr gly OPA
241/81 271/91
CGG GCC CGC TGG TGG CTG CCC CCG CCG ACG ACA GTC CGG GCT GCA GTC CGT CGG ACT ACG
arg ala arg trp trp leu pro pro pro thr thr val arg ala ala val arg arg thr thr
301/101 331/111
ACA GGC TGC CGG TGT CCG GTG CGG TGG TGC TGG TAG ATC
thr gly cys arg cys pro val arg trp cys trp AMB ile

SEQ ID No.19B'

FIGURE 19B'

1/1 31/11
ATC GAA ACT GCA GGA CAT CGC CAA CGC CAA CGA CGG CAC TCG CGC GGT GGG CAC CCC TGG
ile glu thr ala gly his arg gln arg gln arg arg his ser arg gly gly his pro trp
61/21 91/31
CTA TCA GGC CAG CGT CGA CTA TGT GGT AAA CAC ACT GCG CAA CAG CGG TTT TGA TGT GCA
leu ser gly gln arg arg leu cys gly lys his thr ala gln gln arg phe OPA cys ala
121/41 151/51
AAC CCC GGA GTT CTC CGC TCG CGT GTT CAA GGC CGA AAA AGG GGT GGT GAC CCT CGG CGG
asn pro gly val leu arg ser arg val gln gly arg lys arg gly gly asp pro arg arg
181/61 211/71
CAA CAC CGT GGA GGC GAG GGC GCT CGA GTA CAG CCT CGG CAC ACC GCC GGA CGG GGT GAC
gln his arg gly gly glu gly ala arg val gln pro arg his thr ala gly arg gly asp
241/81 271/91
GGG CCC GCT GGT GGC TGC CCC CGC CGA CGA CAG TCC GGG CTG CAG TCC GTC GGA CTA CGA
gly pro ala gly gly cys pro arg arg arg gln ser gly leu gln ser val gly leu arg
301/101 331/111
CAG GCT GCC GGT GTC CGG TGC GGT GGT GCT GGT AGA TC
gln ala ala gly val arg cys gly gly ala gly arg

SEQ ID No.19C'

FIGURE 19C'

sequence Rv0418 predicted by Cole et al. (Nature 393:537-544) and containing seq19A'

1/1	31/11
atg gtg aac aaa tcc agg atg atg ccg gcg	gtg ctg gcc gtg gct gtg gtc gtc gca ttc
Met val asn lys ser arg met met pro ala	val leu ala val ala val val ala phe
61/21	91/31
ctg acg acg ggc tgt atc ccg tgg tct acg	cag tcg ccg ccc gtt gtt aac ggc ccc gct
leu thr thr gly cys ile arg trp ser thr	gln ser arg pro val val asn gly pro ala
121/41	151/51
gcc gca gag ttc gcc gtt gcg ttg cgc aac	cgg gtg agc acc gac gcg atg atg gcg cac
ala ala glu phe ala val ala leu arg asn	arg val ser thr asp ala met met ala his
181/61	211/71
cta tcg aaa ctg cag gac atc gcc aac gcc	aac gac ggc act cgc gcg gtg ggc acc cct
leu ser lys leu gln asp ile ala asn ala	asn asp gly thr arg ala val gly thr pro
241/81	271/91
ggc tat cag gcc agc gtc gac tat gtg gta	aac aca ctg cgc aac agc ggt ttt gat gtg
gly tyr gln ala ser val asp tyr val val	asn thr leu arg asn ser gly phe asp val
301/101	331/111
caa acc ccg gag ttc tcc gct cgc gtg ttc	aag gcc gaa aaa ggg gtg gtg acc ctc ggc
gln thr pro glu phe ser ala arg val phe	lys ala glu lys gly val val thr leu gly
361/121	391/131
ggc aac acc gtg gag gcg agg gcg ctc gag	tac agc ctc ggc aca ccg ccg gac ggc gtg
gly asn thr val glu ala arg ala leu glu	tyr ser leu gly thr pro pro asp gly val
421/141	451/151
acg ggc ccg ctg gtg gct gcc ccc gcc gac	gac agt ccg ggc tgc agt ccg tcg gac tac
thr gly pro leu val ala ala pro ala asp	asp ser pro gly cys ser pro ser asp tyr
481/161	511/171
gac agg ctg ccg gtg tcc ggt gcg gtg gtg	ctg gta gat cgc ggc gtc tgt cct ttt gcc
asp arg leu pro val ser gly ala val val	leu val asp arg gly val cys pro phe ala
541/181	571/191
cag aag gaa gac gca gcc gcg cag cgc ggt	gcg gtg gcg ctg atc att gct gac aac atc
gln lys glu asp ala ala ala gln arg gly	ala val ala leu ile ile ala asp asn ile
601/201	631/211
gac gag cag gcg atg ggc ggc acc ctg ggg	gct aat acc gac gtc aag atc ccg gtg gtg
asp glu gln ala met gly gly thr leu gly	ala asn thr asp val lys ile pro val val
661/221	691/231
agt gtc acc aag tcg gtc gga ttc cag cta	cgc gga cag tct ggg cca acc acc gtc aag
ser val thr lys ser val gly phe gln leu	arg gly gln ser gly pro thr thr val lys
721/241	751/251
ctc acg gcg agc acc caa agt ttc aag gcc	cgc aac gtc atc gcg cag acg aag acg ggc
leu thr ala ser thr gln ser phe lys ala	arg asn val ile ala gln thr lys thr gly
781/261	811/271
tcg tcg gcc aac gtg gtg atg gca ggt gcg	cat ttg gac agc gtt ccg gaa gga ccc ggc
ser ser ala asn val val met ala gly ala	his leu asp ser val pro glu gly pro gly
841/281	871/291
atc aac gac aac ggc tcg gga gtg gct gcg	gtt ctg gaa acg gca gtg cag ctg ggg aac
ile asn asp asn gly ser gly val ala ala	val leu glu thr ala val gln leu gly asn
901/301	931/311
tca ccg cat gtg tcc aac gcg gta ccg ttc	gcc ttc tgg ggc gcc gag gaa ttc ggc ctg
ser pro his val ser asn ala val arg phe	ala phe trp gly ala glu glu phe gly leu
961/321	991/331
att ggg tca cga aac tac gtc gag tcg ctg	gac atc gac gcg ctc aaa ggc atc gcg ctg
ile gly ser arg asn tyr val glu ser leu	asp ile asp ala leu lys gly ile ala leu

SEQ ID No.19 D

FIGURE 19D

ORF according to Cole et al. (Nature 393:537-544) and containing Rv0418

1/1	31/11
tag gcc att caa cgc tct gtt cgt ttg att	ggt cgg tgg gat gcg aaa gct gcg cgg cga
AMB ala ile gln arg ser val arg leu ile	gly arg trp asp ala lys ala ala arg arg
61/21	91/31
cag gcg cgg tct aat ctg ggc gcg atg gtg	aac aaa tcc agg atg atg ccg gcg gtg ctg
gln ala arg ser asn leu gly ala met val	asn lys ser arg met met pro ala val leu
121/41	151/51
gcc gtg gct gtg gtc gtc gca ttc ctg acg	acg ggc tgt atc cgg tgg tct acg cag tcg
ala val ala val val val ala phe leu thr	thr gly cys ile arg trp ser thr gln ser
181/61	211/71
cgg ccc gtt gtt aac ggc ccc gct gcc gca	gag ttc gcc gtt gcg ttg cgc aac cgg gtg
arg pro val val asn gly pro ala ala ala	glu phe ala val ala leu arg asn arg val
241/81	271/91
agc acc gac gcg atg atg gcg cac cta tcg	aaa ctg cag gac atc gcc aac gcc aac gac
ser thr asp ala met met ala his leu ser	lys leu gln asp ile ala asn ala asn asp
301/101	331/111
ggc act cgc gcg gtg ggc acc cct ggc tat	cag gcc agc gtc gac tat gtg gta aac aca
gly thr arg ala val gly thr pro gly tyr	gln ala ser val asp tyr val val asn thr
361/121	391/131
ctg cgc aac agc ggt ttt gat gtg caa acc	ccg gag ttc tcc gct cgc gtg ttc aag gcc
leu arg asn ser gly phe asp val gln thr	pro glu phe ser ala arg val phe lys ala
421/141	451/151
gaa aaa ggg gtg gtg acc ctc ggc ggc aac	acc gtg gag gcg agg gcg ctc gag tac agc
glu lys gly val val thr leu gly gly asn	thr val glu ala arg ala leu glu tyr ser
481/161	511/171
ctc ggc aca ccg ccg gac ggg gtg acg ggc	ccg ctg gtg gct gcc ccc gcc gac gac agt
leu gly thr pro pro asp gly val thr gly	pro leu val ala ala pro ala asp asp ser
541/181	571/191
ccg ggc tgc agt ccg tcg gac tac gac agg	ctg ccg gtg tcc ggt gcg gtg gtg ctg gta
pro gly cys ser pro ser asp tyr asp arg	leu pro val ser gly ala val val leu val
601/201	631/211
gat cgc ggc gtc tgt cct ttt gcc cag aag	gaa gac gca gcc gcg cag cgc ggt gcg gtg
asp arg gly val cys pro phe ala gln lys	glu asp ala ala ala gln arg gly ala val
661/221	691/231
gcg ctg atc att gct gac aac atc gac gag	cag gcg atg ggc ggc acc ctg ggg gct aat
ala leu ile ile ala asp asn ile asp glu	gln ala met gly gly thr leu gly ala asn
721/241	751/251
acc gac gtc aag atc ccg gtg gtg agt gtc	acc aag tcg gtc gga ttc cag cta cgc gga
thr asp val lys ile pro val val ser val	thr lys ser val gly phe gln leu arg gly
781/261	811/271
cag tct ggg cca acc acc gtc aag ctc acg	gcg agc acc caa agt ttc aag gcc cgc aac
gln ser gly pro thr thr val lys leu thr	ala ser thr gln ser phe lys ala arg asn
841/281	871/291
gtc atc gcg cag acg aag acg ggg tcg tcg	gcc aac gtg gtg atg gca ggt gcg cat ttg
val ile ala gln thr lys thr gly ser ser	ala asn val val met ala gly ala his leu
901/301	931/311
gac agc gtt ccg gaa gga ccc ggc atc aac	gac aac ggc tcg gga gtg gct gcg gtt ctg
asp ser val pro glu gly pro gly ile asn	asp asn gly ser gly val ala ala val leu
961/321	991/331
gaa acg gca gtg cag ctg ggg aac tca ccg	cat gtg tcc aac gcg gta cgg ttc gcc ttc
glu thr ala val gln leu gly asn ser pro	his val ser asn ala val arg phe ala phe

SEQ ID No.19 F

FIGURE 19F

73/185

1021/341
tgg ggc gcc gag gaa ttc ggc ctg att ggg tca cga aac tac gtc gag tcg ctg gac atc
trp gly ala glu glu phe gly leu ile gly ser arg asn tyr val glu ser leu asp ile
1081/361
gac gcg ctc aaa ggc atc gcg ctg tat ctg aac ttc gac atg ttg gcg tcg ccg aac ccg
asp ala leu lys gly ile ala leu tyr leu asn phe asp met leu ala ser pro asn pro
1141/381
ggt tac ttc acc tac gac ggt gac cag tcg ctg ccg cta gac gcc cgc ggt cag ccg gtg
gly tyr phe thr tyr asp gly asp gln ser leu pro leu asp ala arg gly gln pro val
1201/401
gtg ccc gaa ggc tcg gcc ggt atc gag cgc acg ttc gtc gcc tat ctg aag atg gcc ggc
val pro glu gly ser ala gly ile glu arg thr phe val ala tyr leu lys met ala gly
1261/421
aag acc gcg cag gac acc tcg ttc gac ggt cgg tcc gac tac gac ggc ttc acg ctg gcg
lys thr ala gln asp thr ser phe asp gly arg ser asp tyr asp gly phe thr leu ala
1321/441
ggt atc cct tcg ggt ggc ctg ttc tcc ggc gct gag gtc aag aag tcc gcc gag caa gcc
gly ile pro ser gly gly leu phe ser gly ala glu val lys lys ser ala glu gln ala
1381/461
gag ctc tgg ggc ggc acc gcc gac gag cct ttc gat ccc aac tat cac cag aag aca gac
glu leu trp gly gly thr ala asp glu pro phe asp pro asn tyr his gln lys thr asp
1441/481
acc ctg gac cat atc gac cgc acc gcg ctc ggt atc aac ggc gct ggc gtc gcg tac gcg
thr leu asp his ile asp arg thr ala leu gly ile asn gly ala gly val ala tyr ala
1501/501
gtg ggt ttg tat gcg cag gac ctc ggc ggc ccc aac ggg gtt ccg gtc atg gcg gac cgc
val gly leu tyr ala gln asp leu gly gly pro asn gly val pro val met ala asp arg
1561/521
acc cgc cac ctg att gcc aaa ccg tga
thr arg his leu ile ala lys pro OPA

SEQ ID No.19F (continued)

FIGURE 19F (continued)

31/11
CGA GAC AGT GGT GCG GGA CAC TTG AGT TCG GCT GCT AAC GAC GCC AGA GTC GCC CGC TTC
arg asp ser gly ala gly his leu ser ser ala ala asn asp ala arg val ala arg phe
61/21
CGC GGT GTG GGA CTC ACG TTC GGT GAG GGT ACA GCG GAC CTT CGA GCA CGC AAT ATC GTG
arg gly val gly leu thr phe gly glu gly thr ala asp leu arg ala arg asn ile val
121/41
GGC CGG CTG GCA ACC GTC GGT TTC GAC GTT GGT GAC GAC CCC TCG TTC ATG AAT CGT TCT
gly arg leu ala thr val gly phe asp val gly asp asp pro ser phe met asn arg ser
181/61
TGA GCT CCC CGT TTT GCT GGA TGC CCA GGC ACC GCC GGT ACT GCT GCG CTT AAG CTT GTC
OPA ala pro arg phe ala gly cys pro gly thr ala gly thr ala ala leu lys leu val
241/81
GCA CAT GGT GCC GGC AGG GAG GAA CAG TGG GCA AGC AGC TAG CCG CGC TCG CCG CGC TGG
ala his gly ala gly arg glu glu gln trp ala ser ser AMB pro arg ser pro arg trp
301/101
TCG GTG CGT GCA TGC TCG CAG CCG GAT GCA CCA ACG TGG TCG ACG GGA CCG CCG TGG CTG
ser val arg ala cys ser gln pro asp ala pro thr trp ser thr gly pro pro trp leu
361/121
CCG ACA AAT CCG GAC CAC TGC ATC AGG ATC
pro thr asn pro asp his cys ile arg ile

SEQ ID No.20A

FIGURE 20A

REPLACEMENT SHEET (RULE 26)

74/185

32/11
GAG ACA GTG GTG CGG GAC ACT TGA GTT CGG CTG CTA ACG ACG CCA GAG TCG CCC GCT TCC
glu thr val val arg asp thr OPA val arg leu leu thr thr pro glu ser pro ala ser
62/21
GCG GTG TGG GAC TCA CGT TCG GTG AGG GTA CAG CGG ACC TTC GAG CAC GCA ATA TCG TGG
ala val trp asp ser arg ser val arg val gln arg thr phe glu his ala ile ser trp
122/41
GCC GGC TGG CAA CCG TCG GTT TCG ACG TTG GTG ACG ACC CCT CGT TCA TGA ATC GTT CTT
ala gly trp gln pro ser val ser thr leu val thr thr pro arg ser OPA ile val leu
182/61
GAG CTC CCC GTT TTG CTG GAT GCC CAG GCA CCG CCG GTA CTG CTG CGC TTA AGC TTG TCG
glu leu pro val leu leu asp ala gln ala pro pro val leu leu arg leu ser leu ser
242/81
CAC ATG GTG CCG GCA GGG AGG AAC AGT GGG CAA GCA GCT AGC CGC GCT CGC CGC GCT GGT
his met val pro ala gly arg asn ser gly gln ala ala ser arg ala arg arg ala gly
302/101
CGG TGC GTG CAT GCT CGC AGC CGG ATG CAC CAA CGT GGT CGA CGG GAC CGC CGT GGC TGC
arg cys val his ala arg ser arg met his gln arg gly arg arg asp arg arg gly cys
362/121
CGA CAA ATC CGG ACC ACT GCA TCA GGA TC
arg gln ile arg thr thr ala ser gly

SEQ ID No.20B

FIGURE 20B

33/11
AGA CAG TGG TGC GGG ACA CTT GAG TTC GGC TGC TAA CGA CGC CAG AGT CGC CCG CTT CCG
arg gln trp cys gly thr leu glu phe gly cys OCH arg arg gln ser arg pro leu pro
63/21
CGG TGT GGG ACT CAC GTT CGG TGA GGG TAC AGC GGA CCT TCG AGC ACG CAA TAT CGT GGG
arg cys gly thr his val arg OPA gly tyr ser gly pro ser ser thr gln tyr arg gly
123/41
CCG GCT GGC AAC CGT CGG TTT CGA CGT TGG TGA CGA CCC CTC GTT CAT GAA TCG TTC TTG
pro ala gly asn arg arg phe arg arg trp OPA arg pro leu val his glu ser phe leu
183/61
AGC TCC CCG TTT TGC TGG ATG CCC AGG CAC CGC CGG TAC TGC TGC GCT TAA GCT TGT CGC
ser ser pro phe cys trp met pro arg his arg arg tyr cys cys ala OCH ala cys arg
243/81
ACA TGG TGC CGG CAG GGA GGA ACA GTG GGC AAG CAG CTA GCC GCG CTC GCC GCG CTG GTC
thr trp cys arg gln gly gly thr val gly lys gln leu ala ala leu ala ala leu val
303/101
GGT GCG TGC ATG CTC GCA GCC GGA TGC ACC AAC GTG GTC GAC GGG ACC GCC GTG GCT GCC
gly ala cys met leu ala ala gly cys thr asn val val asp gly thr ala val ala ala
363/121
GAC AAA TCC GGA CCA CTG CAT CAG GAT C
asp lys ser gly pro leu his gln asp

SEQ ID No.20C

FIGURE 20C

REPLACEMENT SHEET (RULE 26)

part of the nucleotide sequence of seq20A

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1/1                               31/11
TGT GGG ACT CAC GTT CGG TGA GGG TAC AGC GGA CCT TCG AGC ACG CAA TAT CGT GGG CCG
cys gly thr his val arg OPA gly tyr ser gly pro ser ser thr gln tyr arg gly pro
61/21                               91/31
GCT GGC AAC CGT CGG TTT CGA CGT TGG TGA CGA CCC CTC GTT CAT GAA TCG TTC TTG AGC
ala gly asn arg arg phe arg arg trp OPA arg pro leu val his glu ser phe leu ser
121/41                               151/51
TCC CCG TTT TGC TGG ATG CCC AGG CAC CGC CGG TAC TGC TGC GCT TAA GCT TGT CGC ACA
ser pro phe cys trp met pro arg his arg arg tyr cys cys ala OCH ala cys arg thr
181/61                               211/71
TGG TGC CGG CAG GGA GGA ACA GTG GGC AAG CAG CTA GCC GCG CTC GCC GCG CTG GTC GGT
trp cys arg gln gly gly thr val gly lys gln leu ala ala leu ala ala leu val gly
241/81                               271/91
GCG TGC ATG CTC GCA GCC GGA TGC ACC AAC GTG GTC GAC GGG ACC GCC GTG GCT GCC GAC
ala cys met leu ala ala gly cys thr asn val val asp gly thr ala val ala ala asp
301/101
AAA TCC GGA CCA CTG CAT CAG GAT C
lys ser gly pro leu his gln asp

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SEQ ID No.20A'

FIGURE 20A'

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1/1                               31/11
GTG GGA CTC ACG TTC GGT GAG GGT ACA GCG GAC CTT CGA GCA CGC AAT ATC GTG GGC CCG
val gly leu thr phe gly glu gly thr ala asp leu arg ala arg asn ile val gly arg
61/21                               91/31
CTG GCA ACC GTC GGT TTC GAC GTT GGT GAC GAC CCC TCG TTC ATG AAT CGT TCT TGA GCT
leu ala thr val gly phe asp val gly asp asp pro ser phe met asn arg ser OPA ala
121/41                               151/51
CCC CGT TTT GCT GGA TGC CCA GGC ACC GCC GGT ACT GCT GCG CTT AAG CTT GTC GCA CAT
pro arg phe ala gly cys pro gly thr ala gly thr ala ala leu lys leu val ala his
181/61                               211/71
GGT GCC GGC AGG GAG GAA CAG TGG GCA AGC AGC TAG CCG CGC TCG CCG CGC TGG TCG GTG
gly ala gly arg glu glu gln trp ala ser ser AMB pro arg ser pro arg trp ser val
241/81                               271/91
CGT GCA TGC TCG CAG CCG GAT GCA CCA ACG TGG TCG ACG GGA CCG CCG TGG CTG CCG ACA
arg ala cys ser gln pro asp ala pro thr trp ser thr gly pro pro trp leu pro thr
301/101
AAT CCG GAC CAC TGC ATC AGG ATC
asn pro asp his cys ile arg ile

```

SEQ ID No.20B'

FIGURE 20B'

1/1 31/11
 GTG TGG GAC TCA CGT TCG GTG AGG GTA CAG CGG ACC TTC GAG CAC GCA ATA TCG TGG GCC
 val trp asp ser arg ser val arg val gln arg thr phe glu his ala ile ser trp ala
 61/21 91/31
 GGC TGG CAA CCG TCG GTT TCG ACG TTG GTG ACG ACC CCT CGT TCA TGA ATC GTT CTT GAG
 gly trp gln pro ser val ser thr leu val thr thr pro arg ser OPA ile val leu glu
 121/41 151/51
 CTC CCC GTT TTG CTG GAT GCC CAG GCA CCG CCG GTA CTG CTG CGC TTA AGC TTG TCG CAC
 leu pro val leu leu asp ala gln ala pro pro val leu leu arg leu ser leu ser his
 181/61 211/71
 ATG GTG CCG GCA GGG AGG AAC AGT GGG CAA GCA GCT AGC CGC GCT CGC CGC GCT GGT CGG
 met val pro ala gly arg asn ser gly gln ala ala ser arg ala arg arg ala gly arg
 241/81 271/91
 TGC GTG CAT GCT CGC AGC CGG ATG CAC CAA CGT GGT CGA CGG GAC CGC CGT GGC TGC CGA
 cys val his ala arg ser arg met his gln arg gly arg arg asp arg arg gly cys arg
 301/101
 CAA ATC CGG ACC ACT GCA TCA GGA TC
 gln ile arg thr thr ala ser gly

SEQ ID No.20C'

FIGURE 20C'

sequence Rv3576 predicted by Cole et al. (Nature 393:537-544) and containing seq20A'

1/1 31/11
 atg ggc aag cag cta gcc gcg ctc gcc gcg ctg gtc ggt gcg tgc atg ctc gca gcc gga
 met gly lys gln leu ala ala leu ala ala leu val gly ala cys met leu ala ala gly
 61/21 91/31
 tgc acc aac gtg gtc gac ggg acc gcc gtg gct gcc gac aaa tcc gga cca ctg cat cag
 cys thr asn val val asp gly thr ala val ala ala asp lys ser gly pro leu his gln
 121/41 151/51
 gat ccg ata ccg gtt tca gcg ctt gaa ggg ctg ctt ctc gac ttg agc cag atc aat gcc
 asp pro ile pro val ser ala leu glu gly leu leu leu asp leu ser gln ile asn ala
 181/61 211/71
 gcg ctg ggt gcg aca tcg atg aag gtg tgg ttc aac gcc aag gca atg tgg gac tgg agc
 ala leu gly ala thr ser met lys val trp phe asn ala lys ala met trp asp trp ser
 241/81 271/91
 aag agc gtg gcc gac aag aat tgc ctg gct atc gac ggt cca gca cag gaa aag gtc tat
 lys ser val ala asp lys asn cys leu ala ile asp gly pro ala gln glu lys val tyr
 301/101 331/111
 gcc ggc acc ggg tgg acc gct atg cgc gcc caa cgg ctg gat gac agc atc gat gac tcc
 ala gly thr gly trp thr ala met arg gly gln arg leu asp asp ser ile asp asp ser
 361/121 391/131
 aag aaa cgc gac cac tac gcc att caa gcg gtc gtc gcc ttc ccg acc gca cat gat gcc
 lys lys arg asp his tyr ala ile gln ala val val gly phe pro thr ala his asp ala
 421/141 451/151
 gag gag ttc tac agc tcc tcg gtg caa agc tgg agc agc tgc tcg aac cgc cgg ttt gtc
 glu glu phe tyr ser ser ser val gln ser trp ser ser cys ser asn arg arg phe val
 481/161 511/171
 gaa gtc acc ccc gga cag gac gac gcc gcc tgg act gtg gct gac gtt gtc aac gac aac
 glu val thr pro gly gln asp asp ala ala trp thr val ala asp val val asn asp asn
 541/181 571/191
 ggc atg ctc agt agc tcg cag gtt cag gaa ggc ggc gac gga tgg acc tgc cag cgt gcc
 gly met leu ser ser ser gln val gln glu gly gly asp gly trp thr cys gln arg ala
 601/201 631/211
 ctg act gcg cgc aac aac gtc act atc gac att gtc acg tgc gcc tat agc caa ccg gat
 leu thr ala arg asn asn val thr ile asp ile val thr cys ala tyr ser gln pro asp
 661/221 691/231
 ttg gtg gcg att ggc atc gct aac caa atc gcg gcc aag gtt gct aag cag tag
 leu val ala ile gly ile ala asn gln ile ala ala lys val ala lys gln AMB

SEQ ID No.20D

FIGURE 20D

ORF according to Cole et al. (Nature 393:537-544) and containing Rv3576

1/1	31/11
taa gct tgt cgc aca tgg tgc cgg cag gga	gga aca gtg ggc aag cag cta gcc gcg ctc
OCH ala cys arg thr trp cys arg gln gly	gly thr val gly lys gln leu ala ala leu
61/21	91/31
gcc gcg ctg gtc ggt gcg tgc atg ctc gca	gcc gga tgc acc aac gtg gtc gac ggg acc
ala ala leu val gly ala cys met leu ala	ala gly cys thr asn val val asp gly thr
121/41	151/51
gcc gtg gct gcc gac aaa tcc gga cca ctg	cat cag gat ccg ata ccg gtt tca gcg ctt
ala val ala ala asp lys ser gly pro leu	his gln asp pro ile pro val ser ala leu
181/61	211/71
gaa ggg ctg ctt ctc gac ttg agc cag atc	aat gcc gcg ctg ggt gcg aca tcg atg aag
glu gly leu leu leu asp leu ser gln ile	asn ala ala leu gly ala thr ser met lys
241/81	271/91
gtg tgg ttc aac gcc aag gca atg tgg gac	tgg agc aag agc gtg gcc gac aag aat tgc
val trp phe asn ala lys ala met trp asp	trp ser lys ser val ala asp lys asn cys
301/101	331/111
ctg gct atc gac ggt cca gca cag gaa aag	gtc tat gcc ggc acc ggg tgg acc gct atg
leu ala ile asp gly pro ala gln glu lys	val tyr ala gly thr gly trp thr ala met
361/121	391/131
cgc ggc caa cgg ctg gat gac agc atc gat	gac tcc aag aaa cgc gac cac tac gcc att
arg gly gln arg leu asp asp ser ile asp	asp ser lys lys arg asp his tyr ala ile
421/141	451/151
caa gcg gtc gtc ggc ttc ccg acc gca cat	gat gcc gag gag ttc tac agc tcc tcg gtg
gln ala val val gly phe pro thr ala his	asp ala glu glu phe tyr ser ser ser val
481/161	511/171
caa agc tgg agc agc tgc tcg aac cgc cgg	ttt gtc gaa gtc acc ccc gga cag gac gac
gln ser trp ser ser cys ser asn arg arg	phe val glu val thr pro gly gln asp asp
541/181	571/191
gcc gcc tgg act gtg gct gac gtt gtc aac	gac aac ggc atg ctc agt agc tcg cag gtt
ala ala trp thr val ala asp val val asn	asp asn gly met leu ser ser ser gln val
601/201	631/211
cag gaa ggc ggc gac gga tgg acc tgc cag	cgt gcc ctg act gcg cgc aac aac gtc act
gln glu gly gly asp gly trp thr cys gln	arg ala leu thr ala arg asn asn val thr
661/221	691/231
atc gac att gtc acg tgc gcc tat agc caa	ccg gat ttg gtg gcg att ggc atc gct aac
ile asp ile val thr cys ala tyr ser gln	pro asp leu val ala ile gly ile ala asn
721/241	
caa atc gcg gcc aag gtt gct aag cag tag	
gln ile ala ala lys val ala lys gln	AMB

SEQ ID No.20F

FIGURE 20F

1/1 31/11
 GTC CTG GTC GCC GCG CAA CTG GCC GGT CCC GAT GGA AAG TGT TCA CGA TCG CGC TTC TGC
 val leu val ala ala gln leu ala gly pro asp gly lys cys ser arg ser arg phe cys
 61/21 91/31
 CGC TGG TAG TGG CGA TGG TGT TAG CAG GAT TGC GGG TCG AGG CTG CGA TGG CCA GCA CCA
 arg trp AMB trp arg trp cys AMB gln asp cys gly ser arg leu arg trp pro ala pro
 121/41 151/51
 GCG GCC TGC GGC TGG TCG CCG CGC GCG CCG AAA TGA TAC CCG CGA TCA CGA AAT ACA TGT
 ala ala cys gly trp ser pro arg ala pro lys OPA tyr pro arg ser arg asn thr cys
 181/61 211/71
 CGG CGC TGG ACG TCG CCG TGC TGG CCA GCT CGA CCG GAC ACG ATG TGG AGG GGG CGC AGA
 arg arg trp thr ser pro cys trp pro ala arg pro asp thr met trp arg gly arg arg
 241/81 271/91
 AAA ACT TCA CCG CCC GCA AGT ACG AGC TGC AGA CGC GAC TGG CCG ACA CCG ACG TCA TCG
 lys thr ser pro pro ala ser thr ser cys arg arg asp trp pro thr pro thr ser ser
 301/101 331/111
 CAG ACG TGC GGT CGG GAG TGA ACA CGC TGC TCA ACG GCG GTC AGG CGC TGC TGG ATA AGA
 gln thr cys gly arg glu OPA thr arg cys ser thr ala val arg arg cys trp ile arg
 361/121
 TGC TGG CCG ACA GCA TCG GCT TGC GGG ATC
 cys trp pro thr ala ser ala cys gly ile

SEQ ID No.21A

FIGURE 21A

32/11
 TCC TGG TCG CCG CGC AAC TGG CCG GTC CCG ATG GAA AGT GTT CAC GAT CGC GCT TCT GCC
 ser trp ser pro arg asn trp pro val pro met glu ser val his asp arg ala ser ala
 62/21 92/31
 GCT GGT AGT GGC GAT GGT GTT AGC AGG ATT GCG GGT CGA GGC TGC GAT GGC CAG CAC CAG
 ala gly ser gly asp gly val ser arg ile ala gly arg gly cys asp gly gln his gln
 122/41 152/51
 CGG CCT GCG GCT GGT CGC CGC GCG CGC CGA AAT GAT ACC CGC GAT CAC GAA ATA CAT GTC
 arg pro ala ala gly arg arg ala arg arg asn asp thr arg asp his glu ile his val
 182/61 212/71
 GGC GCT GGA CGT CGC CGT GCT GGC CAG CTC GAC CGG ACA CGA TGT GGA GGG GGC GCA GAA
 gly ala gly arg arg arg ala gly gln leu asp arg thr arg cys gly gly gly ala glu
 242/81 272/91
 AAA CTT CAC CGC CCG CAA GTA CGA GCT GCA GAC GCG ACT GGC CGA CAC CGA CGT CAT CGC
 lys leu his arg pro gln val arg ala ala asp ala thr gly arg his arg arg his arg
 302/101 332/111
 AGA CGT GCG GTC GGG AGT GAA CAC GCT GCT CAA CGG CGG TCA GGC GCT GCT GGA TAA GAT
 arg arg ala val gly ser glu his ala ala gln arg arg ser gly ala ala gly OCH asp
 362/121
 GCT GGC CGA CAG CAT CGG CTT GCG GGA TC
 ala gly arg gln his arg leu ala gly

SEQ ID No.21B

FIGURE 21B

79/185

33/11
CCT GGT CGC CGC GCA ACT GGC CGG TCC CGA TGG AAA GTG TTC ACG ATC GCG CTT CTG CCG
pro gly arg arg ala thr gly arg ser arg trp lys val phe thr ile ala leu leu pro
63/21
CTG GTA GTG GCG ATG GTG TTA GCA GGA TTG CGG GTC GAG GCT GCG ATG GCC AGC ACC AGC
leu val val ala met val leu ala gly leu arg val glu ala ala met ala ser thr ser
123/41
GGC CTG CGG CTG GTC GCC GCG CGC GCC GAA ATG ATA CCC GCG ATC ACG AAA TAC ATG TCG
gly leu arg leu val ala ala arg ala glu met ile pro ala ile thr lys tyr met ser
183/61
GCG CTG GAC GTC GCC GTG CTG GCC AGC TCG ACC GGA CAC GAT GTG GAG GGG GCG CAG AAA
ala leu asp val ala val leu ala ser ser thr gly his asp val glu gly ala gln lys
243/81
AAC TTC ACC GCC CGC AAG TAC GAG CTG CAG ACG CGA CTG GCC GAC ACC GAC GTC ATC GCA
asn phe thr ala arg lys tyr glu leu gln thr arg leu ala asp thr asp val ile ala
303/101
GAC GTG CGG TCG GGA GTG AAC ACG CTG CTC AAC GGC GGT CAG GCG CTG CTG GAT AAG ATG
asp val arg ser gly val asn thr leu leu asn gly gly gln ala leu leu asp lys met
363/121
CTG GCC GAC AGC ATC GGC TTG CGG GAT C
leu ala asp ser ile gly leu arg asp

SEQ ID No.21C

FIGURE 21C

part of the nucleotide sequence of seq21A

1/1
ACG ATC GCG CTT CTG CCG CTG GTA GTG GCG ATG GTG TTA GCA GGA TTG CGG GTC GAG GCT
thr ile ala leu leu pro leu val val ala met val leu ala gly leu arg val glu ala
61/21
GCG ATG GCC AGC ACC AGC GGC CTG CGG CTG GTC GCC GCG CGC GCC GAA ATG ATA CCC GCG
ala met ala ser thr ser gly leu arg leu val ala ala arg ala glu met ile pro ala
121/41
ATC ACG AAA TAC ATG TCG GCG CTG GAC GTC GCC GTG CTG GCC AGC TCG ACC GGA CAC GAT
ile thr lys tyr met ser ala leu asp val ala val leu ala ser ser thr gly his asp
181/61
GTG GAG GGG GCG CAG AAA AAC TTC ACC GCC CGC AAG TAC GAG CTG CAG ACG CGA CTG GCC
val glu gly ala gln lys asn phe thr ala arg lys tyr glu leu gln thr arg leu ala
241/81
GAC ACC GAC GTC ATC GCA GAC GTG CGG TCG GGA GTG AAC ACG CTG CTC AAC GGC GGT CAG
asp thr asp val ile ala asp val arg ser gly val asn thr leu leu asn gly gly gln
301/101
GCG CTG CTG GAT AAG ATG CTG GCC GAC AGC ATC GGC TTG CGG GAT C
ala leu leu asp lys met leu ala asp ser ile gly leu arg asp

SEQ ID No.21A'

FIGURE 21A'

sequence Rv3365c predicted by Cole et al. (Nature 393:537-544) and containing Seq21A'

1/1	31/11
gtg acc atg ttc gcc cgc ccg acc atc ccg	gtc gcg gcg gcc gct tct gat att tcc gcc
val thr met phe ala arg pro thr ile pro	val ala ala ala ala ser asp ile ser ala
61/21	91/31
ccg gct caa ccg gcc cgc ggc aaa cct cag	caa cgc ccg ccg tcc tgg tcg ccg cgc aac
pro ala gln pro ala arg gly lys pro gln	gln arg pro pro ser trp ser pro arg asn
121/41	151/51
tgg ccg gtc cga tgg aaa gtg ttc acg atc	gcg ctt ctg ccg ctg gta gtg gcg atg gtg
trp pro val arg trp lys val phe thr ile	ala leu leu pro leu val val ala met val
181/61	211/71
tta gca gga ttg cgg gtc gag gct gcg atg	gcc agc acc agc ggc ctg ccg ctg gtc gcc
leu ala gly leu arg val glu ala ala met	ala ser thr ser gly leu arg leu val ala
241/81	271/91
gcg cgc gcc gaa atg ata ccc gcg atc acg	aaa tac atg tcg gcg ctg gac gtc gcc gtg
ala arg ala glu met ile pro ala ile thr	lys tyr met ser ala leu asp val ala val
301/101	331/111
ctg gcc agc tcg acc gga cac gat gtg gag	ggg gcg cag aaa aac ttc acc gcc cgc aag
leu ala ser ser thr gly his asp val glu	gly ala gln lys asn phe thr ala arg lys
361/121	391/131
tac gag ctg cag acg cga ctg gcc gac acc	gac gtc atc gca gac gtg ccg tcg gga gtg
tyr glu leu gln thr arg leu ala asp thr	asp val ile ala asp val arg ser gly val
421/141	451/151
aac acg ctg ctc aac ggc ggt cag gcg ctg	ctg gat aag gtg ctg gcc gac agc atc ggc
asn thr leu leu asn gly gly gln ala leu	leu asp lys val leu ala asp ser ile gly
481/161	511/171
ttg ccg gat ccg gtc acc gcc tac gcg ccg	ctg ctg ttg acg gcc cag aac gtg att gac
leu arg asp arg val thr ala tyr ala pro	leu leu leu thr ala gln asn val ile asp
541/181	571/191
gcg tcg gtg ccg gtt gac agc gag caa atc	cga acc cag gtg cag ggt ttg agc cga gcc
ala ser val arg val asp ser glu gln ile	arg thr gln val gln gly leu ser arg ala
601/201	631/211
gtt ggc gcc cgc ggg cag atg acg atg cag	gag atc ctg gtg act cgc ggc gcc gac ctt
val gly ala arg gly gln met thr met gln	glu ile leu val thr arg gly ala asp leu
661/221	691/231
gcc gag ccg caa ctg cgc agc gcg atg gtt	acc ctg gcc ggc acc gaa ccc tcg acg ctg
ala glu pro gln leu arg ser ala met val	thr leu ala gly thr glu pro ser thr leu
721/241	751/251
ttc ggg atg agc gcg gcg ctc ggt gca ggc	tcg ccg gac acc aag aac ctg cag cag caa
phe gly met ser ala ala leu gly ala gly	ser pro asp thr lys asn leu gln gln gln
781/261	811/271
atg gtg acc agg atg gcg atc atg tcc gat	ccg gcc gtt gca ctg gtc aac aac cca gag
met val thr arg met ala ile met ser asp	pro ala val ala leu val asn asn pro glu
841/281	871/291
ctg ctg cac tcg ata cag atc acc cgc gac	att gcc gag cag gtg atc acc gac acc acc
leu leu his ser ile gln ile thr arg asp	ile ala glu gln val ile thr asp thr thr
901/301	931/311
gag gcg gtg acg aag tcg gtg caa agc cag	gcc acc gac ccg ccg gat gcc gcg att cgc
glu ala val thr lys ser val gln ser gln	ala thr asp arg arg asp ala ala ile arg
961/321	991/331
gac gcc gtg ctg gtg ttg gcc gcc atc gcg	acc gcg atc gtc gtc gtg ttg gtg gtg gcg
asp ala val leu val leu ala ala ile ala	thr ala ile val val val leu val val ala

SEQ ID No.21F

FIGURE 21D

1861/621
 gtc ggg ctg cgc ggt ccg gtg acc ggt gaa
 val gly leu arg gly pro val thr gly glu
 1921/641
 ctg ccg cta gcc gtg ctc gag ggg acg gcc
 leu pro leu ala val leu glu gly thr ala
 1981/661
 gcg atc aag ccg ccg tgt cct gaa ccc gcg
 ala ile lys pro pro cys pro glu pro ala
 2041/681
 atc ggg ccg cta cca ccg gtc acg ttg ctc
 ile gly pro leu pro pro val thr leu leu
 2101/701
 gcc gac gtc ccg gcc cag ccg atg cag cag
 ala asp val pro ala gln pro met gln gln
 2161/721
 gag gat agg ttt caa cag gag ccc aaa caa
 glu asp arg phe gln gln glu pro lys gln
 2221/741
 ccg ccc gcc aaa ccc gcg cca ccg gcg ggc
 pro pro ala lys pro ala pro pro ala gly
 2281/761
 atg ctc tcc gag atg gtg ggt gac ccg cac
 met leu ser glu met val gly asp pro his
 2341/781
 aag tcg gtg tgg gac cac ggc tgg tcg gcg
 lys ser val trp asp his gly trp ser ala
 2401/801
 tcc cgc acg gac tac ggc ctg ccg gtg cgc
 ser arg thr asp tyr gly leu pro val arg
 2461/821
 gcg gtg cct gag gga ccc gat ccg gag cat
 ala val pro glu gly pro asp arg glu his
 2521/841
 ctt cat ccc ggc cga gcg ccg ccg cac gcg
 leu his pro gly arg ala pro arg his ala
 2581/861
 gcc tcc atc agc agc cat ttc ggc ggc gtg
 ala ser ile ser ser his phe gly gly val
 2641/881
 agt cag gga ccc aat cag caa tga
 ser gln gly pro asn gln gln OPA

1891/631
 cag ggc acc ggc acc acc gcc gag gtc tac
 gln gly thr gly thr thr ala glu val tyr
 1951/651
 cca gcg cag ccg cca aag ccg ccg gta ttt
 pro ala gln pro pro lys pro arg val phe
 2011/671
 gcg gcc gat ccg acg gac gtt ccc gcc gcc
 ala ala asp pro thr asp val pro ala ala
 2071/691
 ccg cgc cgt acc ccg ggg tcc agt ggc atc
 pro arg arg thr pro gly ser ser gly ile
 2131/711
 ccg ccg cgc gag ctg aaa aca ccc tgg tgg
 arg arg arg glu leu lys thr pro trp trp
 2191/731
 ccg ccc gca cca gaa ccg cga ccg gcg ccg
 pro pro ala pro glu pro arg pro ala pro
 2251/751
 ccg gtt gat gac gac gtc atc tac ccg ccg
 pro val asp asp asp val ile tyr arg arg
 2311/771
 gag ctg gcc cac agc ccc gat ctg gac tgg
 glu leu ala his ser pro asp leu asp trp
 2371/791
 gcc gcc gag gcc gcg gac aag ccc gtg cag
 ala ala glu ala ala asp lys pro val gln
 2431/811
 gaa ccc ggg gcc ccg tta gtg ccg ggg gcg
 glu pro gly ala arg leu val pro gly ala
 2491/831
 ccg ggt gca gcg cta gca tcc aac ggc gga
 pro gly ala ala leu ala ser asn gly gly
 2551/851
 gct gcg gta cgc gac ccc gac gcg gtt cgt
 ala ala val arg asp pro asp ala val arg
 2611/871

SEQ ID No.21F (continued 2)

FIGURE 21F (continued 2)

87/185

31/11
CTA CGA CAA GGC AAA GGA GCA CAG GGT GAA GCG TGG ACT GAC GGT CGC GGT AGC CGG AGC
leu arg gln gly lys gly ala gln gly glu ala trp thr asp gly arg gly ser arg ser
61/21
CGC CAT TCT GGT CGC AGG TCT TTC CGG ATG TTC AAG CAA CAA GTC GAC TAC AGG AAG CGG
arg his ser gly arg arg ser phe arg met phe lys gln gln val asp tyr arg lys arg
121/41
TGA GAC CAC GAC CGC GGC AGG CAC GAC GGC AAG CCC CGG CGC CGC ATC CGG GCC GAA GGT
OPA asp his asp arg gly arg his asp gly lys pro arg arg arg ile arg ala glu gly
181/61
CGT CAT CGA CGG TAA GGA CCA GAA CGT CAC CGG GTC TGT GGT GTG CAC AAC CGC GGC CGG
arg his arg arg OCH gly pro glu arg his arg val cys gly val his asn arg gly arg
241/81
CAA TGT CAA CAT CGC GAT CGG CGG GGC GGC GAC CGG CAT TGC CGC CGT GCT CAC CGA CGG
gln cys gln his arg asp arg arg gly gly asp arg his cys arg arg ala his arg arg
301/101
CAA CCC TCC GGA GGT GAA GTC CGT TGG GCT CGG TAA CGT CAA CGG CGT CAC GCT GGG ATA
gln pro ser gly gly glu val arg trp ala arg OCH arg gln arg arg his ala gly ile
361/121
CAC GTC GGG CAC CGG ACA GGG TAA CGC TCG GCA ACC AAG GAC GGC AGC CAC TAC AAG ATC
his val gly his arg thr gly OCH arg ser ala thr lys asp gly ser his tyr lys ile

SEQ ID No.22A

FIGURE 22A

32/11
TAC GAC AAG GCA AAG GAG CAC AGG GTG AAG CGT GGA CTG ACG GTC GCG GTA GCC GGA GCC
tyr asp lys ala lys glu his arg val lys arg gly leu thr val ala val ala gly ala
62/21
GCC ATT CTG GTC GCA GGT CTT TCC GGA TGT TCA AGC AAC AAG TCG ACT ACA GGA AGC GGT
ala ile leu val ala gly leu ser gly cys ser ser asn lys ser thr thr gly ser gly
122/41
GAG ACC ACG ACC GCG GCA GGC ACG ACG GCA AGC CCC GGC GCC GCA TCC GGG CCG AAG GTC
glu thr thr thr ala ala gly thr thr ala ser pro gly ala ala ser gly pro lys val
182/61
GTC ATC GAC GGT AAG GAC CAG AAC GTC ACC GGG TCT GTG GTG TGC ACA ACC GCG GCC GGC
val ile asp gly lys asp gln asn val thr gly ser val val cys thr thr ala ala gly
242/81
AAT GTC AAC ATC GCG ATC GGC GGG GCG GCG ACC GGC ATT GCC GCC GTG CTC ACC GAC GGC
asn val asn ile ala ile gly gly ala ala thr gly ile ala ala val leu thr asp gly
302/101
AAC CCT CCG GAG GTG AAG TCC GTT GGG CTC GGT AAC GTC AAC GGC GTC ACG CTG GGA TAC
asn pro pro glu val lys ser val gly leu gly asn val asn gly val thr leu gly tyr
362/121
ACG TCG GGC ACC GGA CAG GGT AAC GCT CGG CAA CCA AGG ACG GCA GCC ACT ACA AGA TC
thr ser gly thr gly gln gly asn ala arg gln pro arg thr ala ala thr thr arg

SEQ ID No.22B

FIGURE 22B

FIGURE 22C

SEQ ID No.23A

FIGURE 23A

32/11
 CAC AAC CGC GGC CGG CAA TGT CAA CAT CGC GAT CGG CGG GGC GGC GAC CGG CAT TGC CGC
 his asn arg gly arg gln cys gln his arg asp arg arg gly gly asp arg his cys arg
 62/21
 CGT GCT CAC CGA CGG CAA CCC TCC GGA GGT GAA GTC CGT TGG GCT CGG TAA CGT CAA CGG
 arg ala his arg arg gln pro ser gly gly glu val arg trp ala arg OCH arg gln arg
 122/41
 CGT CAC GCT GGG ATA CAC GTC GGG CAC CGG ACA GGG TAA CGC CTC GGC AAC CAA GGA CGG
 arg his ala gly ile his val gly his arg thr gly OCH arg leu gly asn gln gly arg
 182/61
 CAG CCA CTA CAA GAT CAC AGG GTG AAG CGT GGA CTG ACG GTC GCG GTA GCC GGA GCC GCC
 gln pro leu gln asp his arg val lys arg gly leu thr val ala val ala gly ala ala
 242/81
 ATT CTG GTC GCA GGT CTT TCC GGA TGT TCA AGC AAC AAG TCG ACT ACA GGA AGC GGT GAG
 ile leu val ala gly leu ser gly cys ser ser asn lys ser thr thr gly ser gly glu
 302/101
 ACC ACG ACC GCG GCA GGC ACG ACG GCA AGC CCC GGC GCC GCT CCG GGC CGA AGG TCG TCA
 thr thr thr ala ala gly thr thr ala ser pro gly ala ala pro gly arg arg ser ser
 362/121
 TCG ACG GTA AGG ACC AGA ACG TCA CCG GCT CCG TGG TGT GCA CAA CCG CGG CCG GCA ATG
 ser thr val arg thr arg thr ser pro ala pro trp cys ala gln pro arg pro ala met
 422/141
 TCA ACA TCG CGA TCG GCG GGG CGG CGA CCG GCA TTG CCG CCG TGC TCA CCG ACG GCA ACC
 ser thr ser arg ser ala gly arg arg pro ala leu pro pro cys ser pro thr ala thr
 482/161
 CTC CGG AGG TGA AGT CCG TTG GGC TCG GTA ACG TCA ACG GCG TCA CGC TGG GAT ACA CGT
 leu arg arg OPA ser pro leu gly ser val thr ser thr ala ser arg trp asp thr arg
 542/181
 CGG GCA CCG GAC AGG GTA ACG CCT CGG CAA CCA AGG ACG GCA GCC ACT ACA AGA TC
 arg ala pro asp arg val thr pro arg gln pro arg thr ala ala thr thr arg

SEQ ID No.23B

FIGURE 23B

33/11
 ACA ACC GCG GCC GGC AAT GTC AAC ATC GCG ATC GGC GGG GCG GCG ACC GGC ATT GCC GCC
 thr thr ala ala gly asn val asn ile ala ile gly gly ala ala thr gly ile ala ala
 63/21
 GTG CTC ACC GAC GGC AAC CCT CCG GAG GTG AAG TCC GTT GGG CTC GGT AAC GTC AAC GGC
 val leu thr asp gly asn pro pro glu val lys ser val gly leu gly asn val asn gly
 123/41
 GTC ACG CTG GGA TAC ACG TCG GGC ACC GGA CAG GGT AAC GCC TCG GCA ACC AAG GAC GGC
 val thr leu gly tyr thr ser gly thr gly gln gly asn ala ser ala thr lys asp gly
 183/61
 AGC CAC TAC AAG ATC ACA GGG TGA AGC GTG GAC TGA CCG TCG CCG TAG CCG CAG CCG CCA
 ser his tyr lys ile thr gly OPA ser val asp OPA arg ser arg AMB pro glu pro pro
 243/81
 TTC TGG TCG CAG GTC TTT CCG GAT GTT CAA GCA ACA AGT CGA CTA CAG GAA GCG GTG AGA
 phe trp ser gln val phe pro asp val gln ala thr ser arg leu gln glu ala val arg
 303/101
 CCA CGA CCG CGG CAG GCA CGA CGG CAA GCC CCG GCG CCG CTC CGG GCC GAA GGT CGT CAT
 pro arg pro arg gln ala arg arg gln ala pro ala pro leu arg ala glu gly arg his
 363/121
 CGA CGG TAA GGA CCA GAA CGT CAC CGG CTC CGT GGT GTG CAC AAC CGC GGC CGG CAA TGT
 arg arg OCH gly pro glu arg his arg leu arg gly val his asn arg gly arg gln cys
 423/141
 CAA CAT CGC GAT CGG CGG GGC GGC GAC CGG CAT TGC CGC CGT GCT CAC CGA CGG CAA CCC
 gln his arg asp arg arg gly gly asp arg his cys arg arg ala his arg arg gln pro
 483/161
 TCC GGA GGT GAA GTC CGT TGG GCT CGG TAA CGT CAA CGG CGT CAC GCT GGG ATA CAC GTC
 ser gly gly glu val arg trp ala arg OCH arg gln arg arg his ala gly ile his val
 543/181
 GGG CAC CGG ACA GGG TAA CGC CTC GGC AAC CAA GGA CGG CAG CCA CTA CAA GAT C
 gly his arg thr gly OCH arg leu gly asn gln gly arg gln pro leu gln asp

SEQ ID No.23C

FIGURE 23C

91/185

31/11
CTA ACG ACA GGC AAA GGA GCA CAG GGT GAA GCG TGG ACT GAC GGT CGC GGT AGC CGG AGC
leu thr thr gly lys gly ala gln gly glu ala trp thr asp gly arg gly ser arg ser
61/21
CGC CAT TCT GGT CGC AGG TCT TTC CGG ATG TTC AAG CAA CAA GTC GAC TAC AGG AAG CGG
arg his ser gly arg arg ser phe arg met phe lys gln gln val asp tyr arg lys arg
121/41
TGA GAC CAC GAC CGC GGC AGG CAC GAC GGC AAG CCC CGG CGC CGC TCC GGG CCG AAG GTC
OPA asp his asp arg gly arg his asp gly lys pro arg arg arg ser gly pro lys val
181/61
GTC ATC GAC GGT AAG GAC CAG AAC GTC ACC GGC TCC GTG GTG TGC ACA ACC GCG GCC GGC
val ile asp gly lys asp gln asn val thr gly ser val val cys thr thr ala ala gly
241/81
AAT GTC AAC ATC GCG ATC GGC GGG GCG GCG ACC GGC ATT GCC GCC GTG CTC ACC GAC GGC
asn val asn ile ala ile gly gly ala ala thr gly ile ala ala val leu thr asp gly
301/101
AAC CCT CCG GAG GTG AAG TCC GTT GGG CTC GGT AAC GTC AAC GGC GTC ACG CTG GGA TAC
asn pro pro glu val lys ser val gly leu gly asn val asn gly val thr leu gly tyr
361/121
ACG TCG GGC ACC GGA CAG GGT AAC GCC TCG GCA ACC AAG GAC GGC AGC CAC TAC AAG ATC
thr ser gly thr gly gln gly asn ala ser ala thr lys asp gly ser his tyr lys ile
391/131

SEQ ID No.24A

FIGURE 24A

32/11
TAA CGA CAG GCA AAG GAG CAC AGG GTG AAG CGT GGA CTG ACG GTC GCG GTA GCC GGA GCC
OCH arg gln ala lys glu his arg val lys arg gly leu thr val ala val ala gly ala
62/21
GCC ATT CTG GTC GCA GGT CTT TCC GGA TGT TCA AGC AAC AAG TCG ACT ACA GGA AGC GGT
ala ile leu val ala gly leu ser gly cys ser ser asn lys ser thr thr gly ser gly
122/41
GAG ACC ACG ACC GCG GCA GGC ACG ACG GCA AGC CCC GGC GCC GCT CCG GGC CGA AGG TCG
glu thr thr thr ala ala gly thr thr ala ser pro gly ala ala pro gly arg arg ser
182/61
TCA TCG ACG GTA AGG ACC AGA ACG TCA CCG GCT CCG TGG TGT GCA CAA CCG CGG CCG GCA
ser ser thr val arg thr arg thr ser pro ala pro trp cys ala gln pro arg pro ala
242/81
ATG TCA ACA TCG CGA TCG GCG GGG CGG CGA CCG GCA TTG CCG CCG TGC TCA CCG ACG GCA
met ser thr ser arg ser ala gly arg arg pro ala leu pro pro cys ser pro thr ala
302/101
ACC CTC CGG AGG TGA AGT CCG TTG GGC TCG GTA ACG TCA ACG GCG TCA CGC TGG GAT ACA
thr leu arg arg OPA ser pro leu gly ser val thr ser thr ala ser arg trp asp thr
362/121
CGT CGG GCA CCG GAC AGG GTA ACG CCT CGG CAA CCA AGG ACG GCA GCC ACT ACA AGA TC
arg arg ala pro asp arg val thr pro arg gln pro arg thr ala ala thr thr arg
392/131

SEQ ID No.24B

FIGURE 24B

33/11
 AAC GAC AGG CAA AGG AGC ACA GGG TGA AGC GTG GAC TGA CGG TCG CGG TAG CCG GAG CCG
 asn asp arg gln arg ser thr gly OPA ser val asp OPA arg ser arg AMB pro glu pro
 63/21
 93/31
 CCA TTC TGG TCG CAG GTC TTT CCG GAT GTT CAA GCA ACA AGT CGA CTA CAG GAA GCG GTG
 pro phe trp ser gln val phe pro asp val gln ala thr ser arg leu gln glu ala val
 123/41
 153/51
 AGA CCA CGA CCG CGG CAG GCA CGA CGG CAA GCC CCG GCG CCG CTC CGG GCC GAA GGT CGT
 arg pro arg pro arg gln ala arg arg gln ala pro ala pro leu arg ala glu gly arg
 183/61
 213/71
 CAT CGA CGG TAA GGA CCA GAA CGT CAC CGG CTC CGT GGT GTG CAC AAC CGC GGC CGG CAA
 his arg arg OCH gly pro glu arg his arg leu arg gly val his asn arg gly arg gln
 243/81
 273/91
 TGT CAA CAT CGC GAT CGG CGG GGC GGC GAC CGG CAT TGC CGC CGT GCT CAC CGA CGG CAA
 cys gln his arg asp arg arg gly qly asp arg his cys arg arg ala his arg arg gln
 303/101
 333/111
 CCC TCC GGA GGT GAA GTC CGT TGG GCT CGG TAA CGT CAA CGG CGT CAC GCT GGG ATA CAC
 pro ser gly gly glu val arg trp ala arg OCH arg gln arg arg his ala gly ile his
 363/121
 393/131
 GTC GGG CAC CGG ACA GGG TAA CGC CTC GGC AAC CAA GGA CGG CAG CCA CTA CAA GAT C
 val gly his arg thr gly OCH arg leu gly asn gln gly arg gln pro leu gln asp

SEQ ID No.24C

FIGURE 24C

Direct primer

5' ACG CGG CGC AGC CTG TTG 3'

SEQ ID No.25

FIGURE 25

Reverse primer

5' CGA CCT TGG GAT TCG CCT 3'

SEQ ID No.26

FIGURE 26

31/11
 CCT ACC AGC AAG AGC CCA GGG CTT CAC AGG ACC TAA AAG GAG TAG CGC CCA TGG GCT TGA
 pro thr ser lys ser pro gly leu his arg thr OCH lys glu AMB arg pro trp ala OPA
 61/21
 TCC AAT TTT CCT TCC GCC CCG TGC AAT ACC ATC TGC AAG ACC AGC GAC GGC CCG TGG TTG
 ser asn phe pro ser ala pro cys asn thr ile cys lys thr ser asp gly pro trp leu
 121/41
 CGG TCG CGC AGC TTG CGG AAA CGG GGT ATG GAC CCT GCC GTA CCG TTG TTG CCA CTT GAT
 arg ser arg ser leu arg lys arg gly met asp pro ala val pro leu leu pro leu asp
 181/61
 GTC GTC GCT CTC CAC CCG TCG GGG GGC GAA AGC CAT TCC GAC ACT GGG ATC CTC AAA ACG
 val val ala leu his pro ser gly gly glu ser his ser asp thr gly ile leu lys thr
 241/81
 TCG GCT GAG TGT CTG CAG GGC TCC GGG GAG CAG CCG ATC ATC ACC ATG TAC GAA CTG AAT
 ser ala glu cys leu gln gly ser gly glu gln pro ile ile thr met tyr glu leu asn
 301/101
 AAG TCC CCC CCG CGC GAC TTC CAG ACA TTT GTT GTG GTT TCG GTT GAG GCC GAG GCG AGG
 lys ser pro pro arg asp phe gln thr phe val val val ser val glu ala glu ala arg
 361/121
 CTC ATT TCG CAG CAA GCG GTC TCC GGG TCG CAG CAT CGT TGC GGC GAT CGC GGC GCA GTC
 leu ile ser gln gln ala val ser gly ser gln his arg cys gly asp arg gly ala val
 421/141
 GTC GGA CGA GTC GTC GTC AAC GAC CAC GAT C
 val gly arg val val val asn asp his asp

SEQ ID No.27A

FIGURE 27A

31/11
 CTA CCA GCA AGA GCC CAG GGC TTC ACA GGA CCT AAA AGG AGT AGC GCC CAT GGG CTT GAT
 leu pro ala arg ala gln gly phe thr gly pro lys arg ser ser ala his gly leu asp
 61/21
 CCA ATT TTC CTT CCG CCC CGT GCA ATA CCA TCT GCA AGA CCA GCG ACG GCC CGT GGT TGC
 pro ile phe leu pro pro arg ala ile pro ser ala arg pro ala thr ala arg gly cys
 121/41
 GGT CGC GCA GCT TGC GGA AAC GGG GTA TGG ACC CTG CCG TAC CGT TGT TGC CAC TTG ATG
 gly arg ala ala cys gly asn gly val trp thr leu pro tyr arg cys cys his leu met
 181/61
 TCG TCG CTC TCC ACC CGT CGG GGG GCG AAA GCC ATT CCG ACA CTG GGA TCC TCA AAA CGT
 ser ser leu ser thr arg arg gly ala lys ala ile pro thr leu gly ser ser lys arg
 241/81
 CGG CTG AGT GTC TGC AGG GCT CCG GGG AGC AGC CGA TCA TCA CCA TGT ACG AAC TGA ATA
 arg leu ser val cys arg ala pro gly ser ser arg ser ser pro cys thr asn OPA ile
 301/101
 AGT CCC CCC CGC GCG ACT TCC AGA CAT TTG TTG TGG TTT CGG TTG AGG CCG AGG CGA GGC
 ser pro pro arg ala thr ser arg his leu leu trp phe arg leu arg pro arg arg gly
 361/121
 TCA TTT CGC AGC AAG CGG TCT CCG GGT CGC AGC ATC GTT GCG GCG ATC GCG GCG CAG TCG
 ser phe arg ser lys arg ser pro gly arg ser ile val ala ala ile ala ala gln ser
 421/141
 TCG GAC GAG TCG TCG TCA ACG ACC ACG ATC
 ser asp glu ser ser ser thr thr thr ile

SEQ ID No.27B

FIGURE 27B

33/11
TAC CAG CAA GAG CCC AGG GCT TCA CAG GAC CTA AAA GGA GTA GCG CCC ATG GGC TTG ATC
tyr gln gln glu pro arg ala ser gln asp leu lys gly val ala pro met gly leu ile
63/21
CAA TTT TCC TTC CGC CCC GTG CAA TAC CAT CTG CAA GAC CAG CGA CGG CCC GTG GTT GCG
gln phe ser phe arg pro val gln tyr his leu gln asp gln arg arg pro val val ala
123/41
GTC GCG CAG CTT GCG GAA ACG GGG TAT GGA CCC TGC CGT ACC GTT GTT GCC ACT TGA TGT
val ala gln leu ala glu thr gly tyr gly pro cys arg thr val val ala thr OPA cys
183/61
CGT CGC TCT CCA CCC GTC GGG GGG CGA AAG CCA TTC CGA CAC TGG GAT CCT CAA AAC GTC
arg arg ser pro pro val gly gly arg lys pro phe arg his trp asp pro gln asn val
243/81
GGC TGA GTG TCT GCA GGG CTC CGG GGA GCA GCC GAT CAT CAC CAT GTA CGA ACT GAA TAA
gly OPA val ser ala gly leu arg gly ala ala asp his his his val arg thr glu OCH
303/101
GTC CCC CCC GCG CGA CTT CCA GAC ATT TGT TGT GGT TTC GGT TGA GGC CGA GGC GAG GCT
val pro pro ala arg leu pro asp ile cys cys gly phe gly OPA gly arg gly glu ala
363/121
CAT TTC GCA GCA AGC GGT CTC CGG GTC GCA GCA TCG TTG CGG CGA TCG CGG CGC AGT CGT
his phe ala ala ser gly leu arg val ala ala ser leu arg arg ser arg arg ser arg
423/141
CGG ACG AGT CGT CGT CAA CGA CCA CGA TC
arg thr ser arg arg gln arg pro arg

SEQ ID No.27C

FIGURE 27C

MKTGTATRRRLAVLIALALPGAVALLAEPSATGASDPCAASEVAR
TVGSVAKSMGDYLDSPETNQVMTAVLQQQVGPVSVASLKAHFANPK
VASDLHALSQPLTDLSTRCSLPISGLQAIGLMQAVQGARR

SEQ ID No.28

FIGURE 28

GTGGGCAAGC	AGCTAGCCGC	GCTCGCCGCG	CTGGTCGGTG	CGTGCATGCT	CGCAGCCGGA	60
TGCACCAACG	TGGTCGACGG	GACCGCCGTG	GCTGCCGACA	AATCCGGACC	ACTGCATCAG	120
GATCCGATAC	CGGTTTCAGC	GCTTGAAGGG	CTGCTTCTCG	ACTTGAGCCA	GATCAATGCC	180
GCGCTGGGTG	CGACATCGAT	GAAGGTGTGG	TTCAACGCCA	AGGCAATGTG	GGACTGGAGC	240
AAGAGCGTGG	CCGACAAGAA	TTGCCTGGCT	ATCGACGGTC	CAGCACAGGA	AAAGGTCTAT	300
GCCGGCACCG	GGTGGACCGC	TATGCGCGGC	CAACGGCTGG	ATGACAGCAT	CGATGACTCC	360
AAGAAACGCG	ACCACTACGC	CATTCAAGCG	GTCGTCGGCT	TCCCGACCGC	ACATGATGCC	420
GAGGAGTTCT	ACAGCTCCTC	GGTGCAAAGC	TGGAGCAGCT	GCTCGAACCG	CCGGTTTGTC	480
GAAGTCACCC	CCGGACAGGA	CGACGCCGCC	TGGACTGTGG	CTGACGTTGT	CAACGACAAC	540
GGCATGCTCA	GTAGCTCGCA	GGTTCAGGAA	GGCGGCGACG	GATGGACCTG	CCAGCGTGCC	600
CTGACTGCGC	GCAACAACGT	CACTATCGAC	ATTGTACAGT	GCGCCTATAG	CCAACCGGAT	660
TTGGTGCGCA	TTGGCATCGC	TAACCAAATC	GCGGCCAAGG	TTGCTAAGCA	GTAG	714

SEQ ID No.29

FIGURE 29

MGKQLAALAALVGACMLAAGCTNVVDGTAVAADKSGPLHQDPIPVFTSALEGLLLDLSQINAALGATS
 MKVWFNAKAMWDWSKSVADKNCLAIDGPAQEKVYAGTGFTWTAMRGQRLDDSIDDSKKRDHYAIQAVV
 GFPTAHDAEEFYSSSVQSWSSCSNRRFVEVTFTPGQDDAAWTVADVNDNGMLSSSQVQEGGDGWTCQ
 RALTARNNVTDIVTCAYSQPDLVFTAIGIANQIAAKVAKQ

SEQ ID No.30

FIGURE 30

1/1	31/11
AGG CGA ATA CCC GCG AGG GCA GCG CGA CGG	CGG CCC TGC CGG CGC CGT GGC TGC TGA ACA
arg arg ile pro ala arg ala ala arg arg	arg pro cys arg arg arg gly cys OPA thr
61/21	91/31
ACA CAT CCC AGC CGC GCA CGC TTC CGG TAT	CGG GCA GGA TAA ACG ACC CCA ACA GCA CGA
thr his pro ser arg ala arg phe arg tyr	ala ala gly OCH thr thr pro thr ala arg
121/41	151/51
ACA CCA GGA TTG CGA CAA CCA AAG CCC TCG	CGC CTG GCT CGA TTT CGC GCG CAA CGC GGC
thr pro gly leu arg gln pro lys pro ser	arg leu ala arg phe arg ala gln arg gly
181/61	211/71
GTT CTG CCG CCT CGA TCT CAG CGC GGA GGG	CGT CGA GAT C
val leu pro pro arg ser gln arg gly gly	arg arg asp

SEQ ID No.31A

FIGURE 31A

1/1	31/11
GGC GAA TAC CCG CGA GGG CAG CGC GAC GGC	GGC CCT GCC GGC GCC GTG GCT GCT GAA CAA
gly glu tyr pro arg gly gln arg asp gly	gly pro ala gly ala val ala ala glu gln
61/21	91/31
CAC ATC CCA GCC GCG CAC GCT TCC GGT ATG	CGG CAG GAT AAA CGA CCC CAA CAG CAC GAA
his ile pro ala ala his ala ser gly met	arg gln asp lys arg pro gln gln his glu
121/41	151/51
CAC CAG GAT TGC GAC AAC CAA AGC CCT CGC	GCC TGG CTC GAT TTC GCG CGC AAC GCG GCG
his gln asp cys asp asn gln ser pro arg	ala trp leu asp phe ala arg asn ala ala
181/61	211/71
TTC TGC CGC CTC GAT CTC AGC GCG GAG GGC	GTC GAG ATC
phe cys arg leu asp leu ser ala glu gly	val glu ile

SEQ ID No.31B

FIGURE 31B

96/185

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1/1                               31/11
GCG AAT ACC CGC GAG GGC AGC GCG ACG GCG GCC CTG CCG GCG CCG TGG CTG CTG AAC AAC
ala asn thr arg glu gly ser ala thr ala ala leu pro ala pro trp leu leu asn asn
61/21                               91/31
ACA TCC CAG CCG CGC ACG CTT CCG GTA TGC GGC AGG ATA AAC GAC CCC AAC AGC ACG AAC
thr ser gln pro arg thr leu pro val cys gly arg ile asn asp pro asn ser thr asn
121/41                               151/51
ACC AGG ATT GCG ACA ACC AAA GCC CTC GCG CCT GGC TCG ATT TCG CGC GCA ACG CGG CGT
thr arg ile ala thr thr lys ala leu ala pro gly ser ile ser arg ala thr arg arg
181/61                               211/71
TCT GCC GCC TCG ATC TCA GCG CGG AGG GCG TCG AGA TC
ser ala ala ser ile ser ala arg arg ala ser arg

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SEQ ID No.31C

FIGURE 31C

ORF according to Cole et al. (Nature 393:537-544) and containing seq31A

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1/1                               31/11
taa acg acc cca aca gca cga aca cca gga ttg cga caa cca aag ccc tcg cgc ctg gct
OCH thr thr pro thr ala arg thr pro gly leu arg gln pro lys pro ser arg leu ala
61/21                               91/31
cga ttt cgc gcg caa cgc ggc gtt ctg ccg cct cga tct cag cgc gga ggg cgt cga gat
arg phe arg ala gln arg gly val leu pro pro arg ser gln arg gly gly arg arg asp
121/41                               151/51
ccc cgg cgt cgt gtt cgt ggc tca tca tct gca tcc tcc ggg ctt ggc cgc gct gac cgg
pro arg arg arg val arg gly ser ser ser ala ser ser gly leu gly arg ala asp arg
181/61                               211/71
cag ccc gac ccc agg cat gcc cag gcc gac ggc gcg ccc cgg ctg ccc ggc ggt gtg cgc
gln pro asp pro arg his ala gln ala asp gly ala pro arg leu pro gly gly val arg
241/81                               271/91
gtc gcc ggc gcg ggt gcg gcg gtg ggt cag gac gcc ggc gtc ggc gat gag gtg gtg cgg
val ala gly ala gly ala ala val gly gln asp ala gly val gly asp glu val val arg
301/101                               331/111
cgc cgc ttc ggt gac ctt cgt ggt gat gac gtc gcc ggg acg cac gcg cgg ctg gcc ggc
arg arg phe gly asp leu arg gly asp asp val ala gly thr his ala arg leu ala gly
361/121                               391/131
ggg gaa gtg cac cag gcg ccc gtc gcg cgc cgc gcc gct cat gcg cgc cgt gac ggt gtc
gly glu val his gln ala pro val ala arg pro pro ala his ala arg arg asp gly val
421/141                               451/151
ctt gcg ccc ttc ccc ggt ggc cac cag cac ctc gac ggc ctg ccc gac cag ggc gcg gtt
leu ala pro phe pro gly gly his gln his leu asp gly leu pro asp gln gly ala val
481/161                               511/171
ggc ttc cag cga gat ttg ctc ctg cag cgc gat cag gcg ttc ata gcg ttc ctg cac aac
gly phe gln arg asp leu leu leu gln arg asp gln ala phe ile ala phe leu his asn
541/181                               571/191
ggc ttt cgg cag ctg tcc gtc gag ttg cgc ggc cgg tgt ccc ggg ccg ctt gga gta ttg
gly phe arg gln leu ser val glu leu arg gly arg cys pro gly pro leu gly val leu
601/201                               631/211
gaa ggt aaa tgc ggc cgc gaa gcg ggc ccg gcg cac cac gtc gag cgt ggc cgc gaa gtc
glu gly lys cys gly arg glu ala gly pro ala his his val glu arg gly arg glu val
661/221                               691/231
ctc ttc ggt ctc ccc ggg gaa acc gac gat cag atc ggt ggt aat cgc ggc atg cgg gat
leu phe gly leu pro gly glu thr asp asp gln ile gly gly asn arg gly met arg asp
721/241                               751/251
ggc cgc ccg cac gcg ctc gat gat gcc gag gta gcg ctc ggc acg ata gga ccg ccg cat
gly arg pro his ala leu asp asp ala glu val ala leu gly thr ile gly pro pro his
781/261                               811/271
cgc gcg cag gat ccg gtc gga tcc gga ctg tag
arg ala gln asp pro val gly ser gly leu AMB

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SEQ ID No.31F

FIGURE 31F

REPLACEMENT SHEET (RULE 26)

97/185

1/1	aga ctg gtg tac acg gag acc aag ctg aac	31/11	tcg gca ttc tcc ttc ggc ggg cct aag tgt
arg leu val tyr thr glu thr lys leu asn		ser ala phe ser phe gly gly pro lys cys	
61/21	cta gtg aag gtc att cag aaa ctg tcg ggc	91/31	ttg agc atc aac cgg ttc atc gcg att gac
leu val lys val ile gln lys leu ser gly		leu ser ile asn arg phe ile ala ile asp	
121/41	ttc gtc ggt ttc gcg cgg atg gtc gag gcc	151/51	ctc ggc ggc gtc gag gta tgc agc acc acc
phe val gly phe ala arg met val glu ala		leu gly gly val glu val cys ser thr thr	
181/61	ccg ttg cgg gac tac gaa ctg ggc acg gtg	211/71	ctg gag cac gcc gga cgc cag gtc att gac
pro leu arg asp tyr glu leu gly thr val		leu glu his ala gly arg gln val ile asp	
241/81	ggg ccg acc gcg ctg aac tat gtg cgc gct	271/91	cgc cag gtc acc acc gag agc aat ggc gac
gly pro thr ala leu asn tyr val arg ala		arg gln val thr thr glu ser asn gly asp	
301/101	tac ggg cgc atc aaa cgc cag cag ttg ttt	331/111	ttg tcg tcg ctg ctg cgt tcg atg atc
tyr gly arg ile lys arg gln gln leu phe		leu ser ser leu leu arg ser met ile	

SEQ ID No.32A

FIGURE 32A

1/1	gac tgg tgt aca cgg aga cca agc tga act	31/11	cgg cat tct cct tcg gcg ggc cta agt gtc
asp trp cys thr arg arg pro ser OPA thr		arg his ser pro ser ala gly leu ser val	
61/21	tag tga agg tca ttc aga aac tgt cgg gct	91/31	tga gca tca acc ggt tca tcg cga ttg act
AMB OPA arg ser phe arg asn cys arg ala		OPA ala ser thr gly ser ser arg leu thr	
121/41	tcg tcg gtt tcg cgc gga tgg tcg agg ccc	151/51	tcg gcg gcg tcg agg tat gca gca cca ccc
ser ser val ser arg gly trp ser arg pro		ser ala ala ser arg tyr ala ala pro pro	
181/61	cgt tgc ggg act acg aac tgg gca cgg tgc	211/71	tgg agc acg ccg gac gcc agg tca ttg acg
arg cys gly thr thr asn trp ala arg cys		trp ser thr pro asp ala arg ser leu thr	
241/81	ggc cga ccg cgc tga act atg tgc gcg ctc	271/91	gcc agg tca cca ccg aga gca atg gcg act
gly arg pro arg OPA thr met cys ala leu		ala arg ser pro pro arg ala met ala thr	
301/101	acg ggc gca tca aac gcc agc agt tgt ttt	331/111	tgt cgt cgc tgc tgc gtt cga tga tc
thr gly ala ser asn ala ser ser cys phe		cys arg arg cys cys val arg OPA	

SEQ ID No.32B

FIGURE 32B

98/185

1/1	31/11
act ggt gta cac gga gac caa gct gaa ctc	ggc att ctc ctt cgg cgg gcc taa gtg tct
thr gly val his gly asp gln ala glu leu	gly ile leu leu arg arg ala OCH val ser
61/21	91/31
agt gaa ggt cat tca gaa act gtc ggg ctt	gag cat caa ccg gtt cat cgc gat tga ctt
ser glu gly his ser glu thr val gly leu	glu his gln pro val his arg asp OPA leu
121/41	151/51
cgt cgg ttt cgc gcg gat ggt cga ggc cct	cgg cgg cgt cga ggt atg cag cac cac ccc
arg arg phe arg ala asp gly arg gly pro	arg arg arg arg gly met gln his his pro
181/61	211/71
gtt gcg gga cta cga act ggg cac ggt gct	gga gca cgc cgg acg cca ggt cat tga cgg
val ala gly leu arg thr gly his gly ala	gly ala arg arg thr pro gly his OPA arg
241/81	271/91
gcc gac cgc gct gaa cta tgt gcg cgc tcg	cca ggt cac cac cga gag caa tgg cga cta
ala asp arg ala glu leu cys ala arg ser	pro gly his his arg glu gln trp arg leu
301/101	331/111
cgg gcg cat caa acg cca gca gtt gtt ttt	gtc gtc gct gct gcg ttc gat gat c
arg ala his gln thr pro ala val val phe	val val ala ala phe asp asp

SEQ ID No.32C

FIGURE 32C

sequence Rv0822c predicted by Cole et al. (Nature 393:537-544) and containing seq 32A

1/1	31/11
atg agt gac ggc gag agc gcc gcg ccg tgg	gca cgg ctc tcc gag tca gca ttc ccc gat
Met ser asp gly glu ser ala ala pro trp	ala arg leu ser glu ser ala phe pro asp
61/21	91/31
ggt gtt gac cga tgg atc acg gta ccg ccc	gcc aca tgg gtg gca gcc cag ggt ccg cgg
gly val asp arg trp ile thr val pro pro	ala thr trp val ala ala gln gly pro arg
121/41	151/51
gac acc cag aat gtc ggc tgt cat gcc acc	ggc gcc gtt agt gtg gcc gat ctg atc gcc
asp thr gln asn val gly cys his ala thr	gly ala val ser val ala asp leu ile ala
181/61	211/71
agg ctc ggc ccc gct ttt cct gac ctc ccc	acg cac cgc cat gtc gcc ccc gaa ccc gag
arg leu gly pro ala phe pro asp leu pro	thr his arg his val ala pro glu pro glu
241/81	271/91
cca tcc ggc cgc gcc ccg aag gtc cac gac	gac gcc gac gac cag cag gac acc gag gct
pro ser gly arg gly pro lys val his asp	asp ala asp asp gln gln asp thr glu ala
301/101	331/111
atc gcc atc ccg gcc cac tcg ctc gag ttc	ctc tcg gag ctt ccc gac ctc cgg gca gcc
ile ala ile pro ala his ser leu glu phe	leu ser glu leu pro asp leu arg ala ala
361/121	391/131
aac tat ccg cgc gcc gac cac gcc cgc cgt	gaa ccc gag cta ccc ggc aag cag cta acc
asn tyr pro arg ala asp his ala arg arg	glu pro glu leu pro gly lys gln leu thr
421/141	451/151
gga tcg gct cga gtg cgg cca ttg cgg atc	cgc cga acg tcg ccc gcg ccc gcc aag cca
gly ser ala arg val arg pro leu arg ile	arg arg thr ser pro ala pro ala lys pro
481/161	511/171
gcg ccg aac tcc ggc cgg cgc ccg atg gtg	ctg gcc gcg cgc tcg ctg gcg gct ctg ttt
ala pro asn ser gly arg arg pro met val	leu ala ala arg ser leu ala ala leu phe
541/181	571/191
gcc gct ctg gcg ttg gcg ctg acc ggc ggg	gca tgg cag tgg agc gcg tcg aag aac agc
ala ala leu ala leu ala leu thr gly gly	ala trp gln trp ser ala ser lys asn ser
601/201	631/211
cgg ctg aac atg gta agc gcg ctc gac ccg	cat tcg ggc gac atc gtc aac ccc agc ggg
arg leu asn met val ser ala leu asp pro	his ser gly asp ile val asn pro ser gly

SEQ ID No.32D

FIGURE 32D

661/221
cag cat ggc gac gag aac ttc ttg ctc gtc ggt atg gac tct cgt gcc ggg gcg aac gcc
gln his gly asp glu asn phe leu leu val gly met asp ser arg ala gly ala asn ala
721/241
aat atc ggc gcc ggc gac gcc gag gac gcc ggc ggc gca cgt tcg gac acc gtc atg ctg
asn ile gly ala gly asp ala glu asp ala gly gly ala arg ser asp thr val met leu
781/261
gtc aac att ccg gcc agc cgc gag cgg gtc gtc gcg gtg tcg ttc ccc cgc gac ctg gcg
val asn ile pro ala ser arg glu arg val val ala val ser phe pro arg asp leu ala
841/281
atc act cca atc caa tgc gag gcg tgg aac ccc gag acc ggt aag tac gga ccc atc tac
ile thr pro ile gln cys glu ala trp asn pro glu thr gly lys tyr gly pro ile tyr
901/301
gac gag aag acg gga acg atg ggt ccc aga ctg gtg tac acg gag acc aag ctg aac tcg
asp glu lys thr gly thr met gly pro arg leu val tyr thr glu thr lys leu asn ser
961/321
gca ttc tcc ttc ggc ggg cct aag tgt cta gtg aag gtc att cag aaa ctg tcg gcc ttg
ala phe ser phe gly gly pro lys cys leu val lys val ile gln lys leu ser gly leu
1021/341
agc atc aac cgg ttc atc gcg att gac ttc gtc ggt ttc gcg cgg atg gtc gag gcc ctc
ser ile asn arg phe ile ala ile asp phe val gly phe ala arg met val glu ala leu
1081/361
ggc ggc gtc gag gta tgc agc acc acc ccg ttg ccg gac tac gaa ctg ggc acg gtg ctg
gly gly val glu val cys ser thr thr pro leu arg asp tyr glu leu gly thr val leu
1141/381
gag cac gcc gga cgc cag gtc att gac ggg ccg acc gcg ctg aac tat gtg cgc gct cgc
glu his ala gly arg gln val ile asp gly pro thr ala leu asn tyr val arg ala arg
1201/401
cag gtc acc acc gag agc aat ggc gac tac ggg cgc atc aaa cgc cag cag ttg ttt ttg
gln val thr thr glu ser asn gly asp tyr gly arg ile lys arg gln gln leu phe leu
1261/421
tcg tcg ctg ctg cgt tcg atg atc tcg acg gac acc ttg ttc aac ctc agc agg ctc aac
ser ser leu leu arg ser met ile ser thr asp thr leu phe asn leu ser arg leu asn
1321/441
aac gtc gtc aac atg ttc atc ggt aac agc tac gtg gac aac gtc aag acc aaa gac ctg
asn val val asn met phe ile gly asn ser tyr val asp asn val lys thr lys asp leu
1381/461
gtc gaa ctc ggt cga tcg ttg cag cat atg gcg gcc ggg cac gtc acg ttc gtg acc gtt
val glu leu gly arg ser leu gln his met ala ala gly his val thr phe val thr val
1441/481
ccg acc ggt ata acc gac cag aac ggc gac gag ccc ccg cgt acc tcc gac atg aag gcg
pro thr gly ile thr asp gln asn gly asp glu pro pro arg thr ser asp met lys ala
1501/501
ctt ttc acc gcc atc atc gac gac gat ccg ctg ccc ctg gaa aac gat cac aac gcc cag
leu phe thr ala ile ile asp asp asp pro leu pro leu glu asn asp his asn ala gln
1561/521
cgt ctg ggc aac acg ccg tcg acc ccg ccg acc acc acc aag aag gcg ccg cag gcg ggt
arg leu gly asn thr pro ser thr pro pro thr thr thr lys lys ala pro gln ala gly
1621/541
ctg acc aac gag att cag cac cag cag gtt acg acg acc tcg cca aaa gag gtc aca gtg
leu thr asn glu ile gln his gln gln val thr thr thr ser pro lys glu val thr val
1681/561
cag gtc tct aac tcg acc ggc cag gcc ggt ttg gcc acc acc gcc acc gat cag ctc aag
gln val ser asn ser thr gly gln ala gly leu ala thr thr ala thr asp gln leu lys
1741/581
cgg aac ggc ttc aac gtg atg gct ccg gac gac tac ccg agt tcg ctg ctg gcc acc aca
arg asn gly phe asn val met ala pro asp asp tyr pro ser ser leu leu ala thr thr
1801/601
gtg ttt ttt tcg ccc ggc aac gaa cag gct gcc gcc acc gtg gcc gcc gtg ttc ggc cag
val phe phe ser pro gly asn glu gln ala ala ala thr val ala ala val phe gly gln
1861/621
tca aag atc gag cgg gtg acc ggg atc ggc caa ctg gtc cag gtg gtg ctg ggc caa gac
ser lys ile glu arg val thr gly ile gly gln leu val gln val val leu gly gln asp

SEQ ID No.32D (continued 1)

FIGURE 32D (continued 1)

REPLACEMENT SHEET (RULE 26)

1921/641
 ttc agc gcg gtg cgc gct ccc ctg ccg agt ggc tcc acc gtc agc gtg cag ata agc cgc
 phe ser ala val arg ala pro leu pro ser gly ser thr val ser val gln ile ser arg
 1981/661
 aac tcc tcc agc cca ccg acc aag ctg ccc gag gac ctg acg gtc acc aac gcc gcc gac
 asn ser ser ser pro pro thr lys leu pro glu asp leu thr val thr asn ala ala asp
 2041/681
 acc acc tgc gag tag
 thr thr cys glu AMB

1951/651

2011/671

SEQ ID No.32D (continued 2)
 FIGURE 32D (continued 2)

ORF according to Cole et al. (Nature 393:537-544) and containing Rv0822c

1/1
 tag gac atg agt gac ggc gag agc gcc gcg ccg tgg gca cgg ctc tcc gag tca gca ttc
 AMB asp met ser asp gly glu ser ala ala pro trp ala arg leu ser glu ser ala phe
 61/21
 ccc gat ggt gtt gac cga tgg atc acg gta ccg ccc gcc aca tgg gtg gca gcc cag ggt
 pro asp gly val asp arg trp ile thr val pro pro ala thr trp val ala ala gln gly
 121/41
 ccg cgg gac acc cag aat gtc ggc tgt cat gcc acc ggc gcc gtt agt gtg gcc gat ctg
 pro arg asp thr gln asn val gly cys his ala thr gly ala val ser val ala asp leu
 181/61
 atc gcc agg ctc ggc ccc gct ttt cct gac ctc ccc acg cac cgc cat gtc gcc ccc gaa
 ile ala arg leu gly pro ala phe pro asp leu pro thr his arg his val ala pro glu
 241/81
 ccc gag cca tcc ggc cgc ggc ccg aag gtc cac gac gac gcc gac gac cag cag gac acc
 pro glu pro ser gly arg gly pro lys val his asp asp ala asp asp gln gln asp thr
 301/101
 gag gct atc gcc atc ccg gcc cac tcg ctc gag ttc ctc tcg gag ctt ccc gac ctc cgg
 glu ala ile ala ile pro ala his ser leu glu phe leu ser glu leu pro asp leu arg
 361/121
 gca gcc aac tat ccg cgc gcc gac cac gcc cgc cgt gaa ccc gag cta ccc ggc aag cag
 ala ala asn tyr pro arg ala asp his ala arg arg glu pro glu leu pro gly lys gln
 421/141
 cta acc gga tcg gct cga gtg ccg cca ttg ccg atc cgc cga acg tcg ccc gcg ccc gcc
 leu thr gly ser ala arg val arg pro leu arg ile arg arg thr ser pro ala pro ala
 481/161
 aag cca gcg ccg aac tcc ggc ccg cgc ccg atg gtg ctg gcc gcg cgc tcg ctg gcg gct
 lys pro ala pro asn ser gly arg arg pro met val leu ala ala arg ser leu ala ala
 541/181
 ctg ttt gcc gct ctg gcg ttg gcg ctg acc ggc ggg gca tgg cag tgg agc gcg tcg aag
 leu phe ala ala leu ala leu ala leu thr gly gly ala trp gln trp ser ala ser lys
 601/201
 aac agc cgg ctg aac atg gta agc gcg ctc gac ccg cat tcg ggc gac atc gtc aac ccc
 asn ser arg leu asn met val ser ala leu asp pro his ser gly asp ile val asn pro
 661/221
 agc ggg cag cat ggc gac gag aac ttc ttg ctc gtc ggt atg gac tct cgt gcc ggg gcg
 ser gly gln his gly asp glu asn phe leu leu val gly met asp ser arg ala gly ala
 721/241
 aac gcc aat atc ggc gcc ggc gac gcc gag gac gcc ggc ggc gca cgt tcg gac acc gtc
 asn ala asn ile gly ala gly asp ala glu asp ala gly gly ala arg ser asp thr val
 781/261
 atg ctg gtc aac att ccg gcc agc cgc gag ccg gtc gtc gcg gtg tcg ttc ccc cgc gac
 met leu val asn ile pro ala ser arg glu arg val val ala val ser phe pro arg asp

SEQ ID No.32F

FIGURE 32F

REPLACEMENT SHEET (RULE 26)

841/281
 ctg gcg atc act cca atc caa tgc gag gcg tgg aac ccc gag acc ggt aag tac gga ccc
 leu ala ile thr pro ile gln cys glu ala trp asn pro glu thr gly lys tyr gly pro
 901/301
 atc tac gac gag aag acg gga acg atg ggt ccc aga ctg gtg tac acg gag acc aag ctg
 ile tyr asp glu lys thr gly thr met gly pro arg leu val tyr thr glu thr lys leu
 961/321
 aac tcg gca ttc tcc ttc ggc ggg cct aag tgt cta gtg aag gtc att cag aaa ctg tcg
 asn ser ala phe ser phe gly gly pro lys cys leu val lys val ile gln lys leu ser
 1021/341
 ggc ttg agc atc aac cgg ttc atc gcg att gac ttc gtc ggt ttc gcg cgg atg gtc gag
 gly leu ser ile asn arg phe ile ala ile asp phe val gly phe ala arg met val glu
 1081/361
 gcc ctc ggc ggc gtc gag gta tgc agc acc acc ccg ttg cgg gac tac gaa ctg ggc acg
 ala leu gly gly val glu val cys ser thr thr pro leu arg asp tyr glu leu gly thr
 1141/381
 gtg ctg gag cac gcc gga cgc cag gtc att gac ggg ccg acc gcg ctg aac tat gtg cgc
 val leu glu his ala gly arg gln val ile asp gly pro thr ala leu asn tyr val arg
 1201/401
 gct cgc cag gtc acc acc gag agc aat ggc gac tac ggg cgc atc aaa cgc cag cag ttg
 ala arg gln val thr thr glu ser asn gly asp tyr gly arg ile lys arg gln gln leu
 1261/421
 ttt ttg tcg tcg ctg ctg cgt tcg atg atc tcg acg gac acc ttg ttc aac ctc agc agg
 phe leu ser ser leu leu arg ser met ile ser thr asp thr leu phe asn leu ser arg
 1321/441
 ctc aac aac gtc gtc aac atg ttc atc ggt aac agc tac gtg gac aac gtc aag acc aaa
 leu asn asn val val asn met phe ile gly asn ser tyr val asp asn val lys thr lys
 1381/461
 gac ctg gtc gaa ctc ggt cga tcg ttg cag cat atg gcg gcc ggg cac gtc acg ttc gtg
 asp leu val glu leu gly arg ser leu gln his met ala ala gly his val thr phe val
 1441/481
 acc gtt ccg acc ggt ata acc gac cag aac ggc gac gag ccc ccg cgt acc tcc gac atg
 thr val pro thr gly ile thr asp gln asn gly asp glu pro pro arg thr ser asp met
 1501/501
 aag gcg ctt ttc acc gcc atc atc gac gac gat ccg ctg ccc ctg gaa aac gat cac aac
 lys ala leu phe thr ala ile ile asp asp asp pro leu pro leu glu asn asp his asn
 1561/521
 gcc cag cgt ctg ggc aac acg ccg tcg acc ccg ccg acc acc acc aag aag gcg ccg cag
 ala gln arg leu gly asn thr pro ser thr pro pro thr thr thr lys lys ala pro gln
 1621/541
 gcg ggt ctg acc aac gag att cag cac cag cag gtt acg acg acc tcg cca aaa gag gtc
 ala gly leu thr asn glu ile gln his gln gln val thr thr thr ser pro lys glu val
 1681/561
 aca gtg cag gtc tct aac tcg acc ggc cag gcc ggt ttg gcc acc acc gcc acc gat cag
 thr val gln val ser asn ser thr gly gln ala gly leu ala thr thr ala thr asp gln
 1741/581
 ctc aag ccg aac ggc ttc aac gtg atg gct ccg gac gac tac ccg agt tcg ctg ctg gcc
 leu lys arg asn gly phe asn val met ala pro asp asp tyr pro ser ser leu leu ala
 1801/601
 acc aca gtg ttt ttt tcg ccc ggc aac gaa cag gct gcc gcc acc gtg gcc gcc gtg ttc
 thr thr val phe phe ser pro gly asn glu gln ala ala ala thr val ala ala val phe
 1861/621
 ggc cag tca aag atc gag ccg gtg acc ggg atc ggc caa ctg gtc cag gtg gtg ctg ggc
 gly gln ser lys ile glu arg val thr gly ile gly gln leu val gln val val leu gly
 1921/641
 caa gac ttc agc gcg gtg cgc gct ccc ctg ccg agt ggc tcc acc gtc agc gtg cag ata
 gln asp phe ser ala val arg ala pro leu pro ser gly ser thr val ser val gln ile
 1981/661
 agc cgc aac tcc tcc agc cca ccg acc aag ctg ccc gag gac ctg acg gtc acc aac gcc
 ser arg asn ser ser ser pro pro thr lys leu pro glu asp leu thr val thr asn ala
 2041/681
 gcc gac acc acc tgc gag tag
 ala asp thr thr cys glu AMB

SEQ ID 32F (continued 1)

FIGURE 32F (continued 1)

REPLACEMENT SHEET (RULE 26)

102/185

1/1 31/11
CGT CAC CTC TGC CAT GGT CCA TCT ACG GTA TCT GCG ACA AGG GCA GCG TCG ATC CCT CGA
arg his leu cys his gly pro ser thr val ser ala thr arg ala ala ser ile pro arg
61/21 91/31
CAT GCA GAG TCG GTG TTC GCT TCA CGC GAA CTA GGC GCG CCT AGC CTG GAC GAG TCC CCG
his ala glu ser val phe ala ser arg glu leu gly ala pro ser leu asp glu ser pro
121/41 151/51
GGC CGA CAT TCG CCC GAG GCC TTG GCC TCC ATC ACC TAA TTG TGT GCA AAA CCG TAT CTA
gly arg his ser pro glu ala leu ala ser ile thr OCH leu cys ala lys pro tyr leu
181/61 211/71
ATT GAT ACG ATT GCG CAC ATG GCT ATC TGG GAT C
ile asp thr ile ala his met ala ile trp asp

SEQ ID No.33A

FIGURE 33A

1/1 31/11
GTC ACC TCT GCC ATG GTC CAT CTA CGG TAT CTG CGA CAA GGG CAG CGT CGA TCC CTC GAC
val thr ser ala met val his leu arg tyr leu arg gln gly gln arg arg ser leu asp
61/21 91/31
ATG CAG AGT CGG TGT TCG CTT CAC GCG AAC TAG GCG CGC CTA GCC TGG ACG AGT CCC CGG
met gln ser arg cys ser leu his ala asn AMB ala arg leu ala trp thr ser pro arg
121/41 151/51
GCC GAC ATT CGC CCG AGG CCT TGG CCT CCA TCA CCT AAT TGT GTG CAA AAC CGT ATC TAA
ala asp ile arg pro arg pro trp pro pro ser pro asn cys val gln asn arg ile OCH
181/61 211/71
TTG ATA CGA TTG CGC ACA TGG CTA TCT GGG ATC
leu ile arg leu arg thr trp leu ser gly ile

SEQ ID No.33B

FIGURE 33B

1/1 31/11
CCG TCA CCT CTG CCA TGG TCC ATC TAC GGT ATC TGC GAC AAG GGC AGC GTC GAT CCC TCG
pro ser pro leu pro trp ser ile tyr gly ile cys asp lys gly ser val asp pro ser
61/21 91/31
ACA TGC AGA GTC GGT GTT CGC TTC ACG CGA ACT AGG CGC GCC TAG CCT GGA CGA GTC CCC
thr cys arg val gly val arg phe thr arg thr arg arg ala AMB pro gly arg val pro
121/41 151/51
GGG CCG ACA TTC GCC CGA GGC CTT GGC CTC CAT CAC CTA ATT GTG TGC AAA ACC GTA TCT
gly pro thr phe ala arg gly leu gly leu his his leu ile val cys lys thr val ser
181/61 211/71
AAT TGA TAC GAT TGC GCA CAT GGC TAT CTG GGA TC
asn OPA tyr asp cys ala his gly tyr leu gly

SEQ ID No.33C

FIGURE 33C

sequence Rv1044 predicted by Cole et al. (Nature 393:537-544) and containing seq33A

1/1	31/11
ttg tgt gca aaa ccg tat cta att gat acg	att gcg cac atg gct atc tgg gat cgc ctc
leu cys ala lys pro tyr leu ile asp thr	ile ala his met ala ile trp asp arg leu
61/21	91/31
gtc gag gtt gcc gcc gag caa cat ggc tac	gtc acg act cgc gat gcg cga gac atc ggc
val glu val ala ala glu gln his gly tyr	val thr thr arg asp ala arg asp ile gly
121/41	151/51
gtc gac cct gtg cag ctc cgc ctc cta gcg	ggg cgc gga cgt ctt gag cgt gtc ggc cga
val asp pro val gln leu arg leu leu ala	gly arg gly arg leu glu arg val gly arg
181/61	211/71
ggg gtg tac cgg gtg ccc gtg ctg ccg cgt	ggg gag cac gac gat ctc gca gcc gca gtg
gly val tyr arg val pro val leu pro arg	gly glu his asp asp leu ala ala ala val
241/81	271/91
tcg tgg act ttg ggg cgt ggc gtt atc tcg	cat gag tcg gcc ttg gcg ctt cat gcc ctc
ser trp thr leu gly arg gly val ile ser	his glu ser ala leu ala leu his ala leu
301/101	331/111
gct gac gtg aac ccg tcg cgc atc cat ctc	acc gtc ccg cgc aac aac cat ccg cgt gcg
ala asp val asn pro ser arg ile his leu	thr val pro arg asn asn his pro arg ala
361/121	391/131
gcc ggg ggc gag ctg tac cga gtt cac cgc	cgc gac ctc cag gca gcc cac gtc act tcg
ala gly gly glu leu tyr arg val his arg	arg asp leu gln ala ala his val thr ser
421/141	451/151
gtc gac gga ata ccc gtc acg acg gtt gcg	cgc acc atc aaa gac tgc gtg aag acg ggc
val asp gly ile pro val thr thr val ala	arg thr ile lys asp cys val lys thr gly
481/161	511/171
acg gat cct tat cag ctt cgg gcc gcg atc	gag cga gcc gaa gcc gag ggc acg ctt cgt
thr asp pro tyr gln leu arg ala ala ile	glu arg ala glu ala glu gly thr leu arg
541/181	571/191
cgt ggg tca gca gct gag cta cgc gct gcg	ctc gat gag acc act gcc gga tta cgc gct
arg gly ser ala ala glu leu arg ala ala	leu asp glu thr thr ala gly leu arg ala
601/201	
cgg ccg aag cga gca tcg gcg tga	
arg pro lys arg ala ser ala OPA	

SEQ ID No.33D

FIGURE 33D

ORF according to Cole et al. (Nature 393:537-544) and containing Rv1044

1/1 31/11
 taa ttg tgt gca aaa ccg tat cta att gat acg att gcg cac atg gct atc tgg gat cgc
 OCH leu cys ala lys pro tyr leu ile asp thr ile ala his met ala ile trp asp arg
 61/21 91/31
 ctc gtc gag gtt gcc gcc gag caa cat ggc tac gtc acg act cgc gat gcg cga gac atc
 leu val glu val ala ala glu gln his gly tyr val thr thr arg asp ala arg asp ile
 121/41 151/51
 ggc gtc gac cct gtg cag ctc cgc ctc cta gcg ggg cgc gga cgt ctt gag cgt gtc ggc
 gly val asp pro val gln leu arg leu leu ala gly arg gly arg leu glu arg val gly
 181/61 211/71
 cga ggt gtg tac cgg gtg ccc gtg ctg ccg cgt ggt gag cac gac gat ctc gca gcc gca
 arg gly val tyr arg val pro val leu pro arg gly glu his asp asp leu ala ala ala
 241/81 271/91
 gtg tcg tgg act ttg ggg cgt ggc gtt atc tcg cat gag tcg gcc ttg gcg ctt cat gcc
 val ser trp thr leu gly arg gly val ile ser his glu ser ala leu ala leu his ala
 301/101 331/111
 ctc gct gac gtg aac ccg tcg cgc atc cat ctc acc gtc ccg cgc aac aac cat ccg cgt
 leu ala asp val asn pro ser arg ile his leu thr val pro arg asn asn his pro arg
 361/121 391/131
 gcg gcc ggg ggc gag ctg tac cga gtt cac cgc cgc gac ctc cag gca gcc cac gtc act
 ala ala gly gly glu leu tyr arg val his arg arg asp leu gln ala ala his val thr
 421/141 451/151
 tcg gtc gac gga ata ccc gtc acg acg gtt gcg cgc acc atc aaa gac tgc gtg aag acg
 ser val asp gly ile pro val thr thr val ala arg thr ile lys asp cys val lys thr
 481/161 511/171
 ggc acg gat cct tat cag ctt cgg gcc gcg atc gag cga gcc gaa gcc gag ggc acg ctt
 gly thr asp pro tyr gln leu arg ala ala ile glu arg ala glu ala glu gly thr leu
 541/181 571/191
 cgt cgt ggg tca gca gct gag cta cgc gct gcg ctc gat gag acc act gcc gga tta cgc
 arg arg gly ser ala ala glu leu arg ala ala leu asp glu thr thr ala gly leu arg
 601/201
 gct cgg ccg aag cga gca tcg gcg tga
 ala arg pro lys arg ala ser ala OPA

SEQ ID No.33F

FIGURE 33F

1/1 31/11
 ATC CAA CCT GCT GGG CCT GCG CCT TCG AAT CGA CGG CCA GGC CAC CGC TCG CTG CCG GCA
 ile gln pro ala gly pro ala pro ser asn arg arg pro gly his arg ser leu pro ala
 61/21 91/31
 ACA ACA CCT GGA ATG GGG ACC TTT TCG GTG TTG CTG GTA ACC GGG ACA ACC GGC ACC ACG
 thr thr pro gly met gly thr phe ser val leu leu val thr gly thr thr gly thr thr
 121/41 151/51
 CCT CGG TCG AGA CGT ATC GCG GCA GCG TTG GCC CTG TCG TTG CTG ACA ATT ACC GCT GGC
 pro arg ser arg arg ile ala ala ala leu ala leu ser leu leu thr ile thr ala gly
 181/61 211/71
 CGC CGC ATA TTT GCC GCG CTG CCG CGG GCC GGA TC
 arg arg ile phe ala ala leu pro arg ala gly

SEQ ID No.34A

FIGURE 34A

105/185

1/1 31/11
TCC AAC CTG CTG GGC CTG CGC CTT CGA ATC GAC GGC CAG GCC ACC GCT CGC TGC CGG CAA
ser asn leu leu gly leu arg leu arg ile asp gly gln ala thr ala arg cys arg gln
61/21 91/31
CAA CAC CTG GAA TGG GGA CCT TTT CGG TGT TGC TGG TAA CCG GGA CAA CCG GCA CCA CGC
gln his leu glu trp gly pro phe arg cys cys trp OCH pro gly gln pro ala pro arg
121/41 151/51
CTC GGT CGA GAC GTA TCG CGG CAG CGT TGG CCC TGT CGT TGC TGA CAA TTA CCG CTG GCC
leu gly arg asp val ser arg gln arg trp pro cys arg cys OPA gln leu pro leu ala
181/61 211/71
GCC GCA TAT TTG CCG CGC TGC CGC GGG CCG GAT C
ala ala tyr leu pro arg cys arg gly pro asp

SEQ ID No.34B

FIGURE 34B

1/1 31/11
GAT CCA ACC TGC TGG GCC TGC GCC TTC GAA TCG ACG GCC AGG CCA CCG CTC GCT GCC GGC
asp pro thr cys trp ala cys ala phe glu ser thr ala arg pro pro leu ala ala gly
61/21 91/31
AAC AAC ACC TGG AAT GGG GAC CTT TTC GGT GTT GCT GGT AAC CCG GAC AAC CCG CAC CAC
asn asn thr trp asn gly asp leu phe gly val ala gly asn arg asp asn arg his his
121/41 151/51
GCC TCG GTC GAG ACG TAT CGC GGC AGC GTT GGC CCT GTC GTT GCT GAC AAT TAC CGC TGG
ala ser val glu thr tyr arg gly ser val gly pro val val ala asp asn tyr arg trp
181/61 211/71
CCG CCG CAT ATT TGC CGC GCT GCC GCG GGC CGG ATC
pro pro his ile cys arg ala ala ala gly arg ile

SEQ ID No.34C

FIGURE 34C

1/1																			31/11				
tag ccg cag ggc cct gcg gct agg cgc ggc																			cgg tgc cgt tgg ccg ccg cgg caa tcg atg				
AMB pro gln gly pro ala ala arg arg gly																			arg cys arg trp pro arg arg gln ser met				
61/21																			91/31				
ttg cag cag tta caa cgc caa atg gag tct																			gag cgc atc gtc gag ttc gat cag ctc ggc				
leu gln gln leu gln arg gln met glu ser																			glu arg ile val glu phe asp gln leu gly				
121/41																			151/51				
agg gga gac gtt gcg cag cga cgg atc caa																			cct gct ggg cct gcg cct tcg aat cga cgg				
arg gly asp val ala gln arg arg ile gln																			pro ala gly pro ala pro ser asn arg arg				
181/61																			211/71				
cca ggc cac cgc tcg ctg ccg gca aca aca																			cct gga atg ggg acc ttt tcg gtg ttg ctg				
pro gly his arg ser leu pro ala thr thr																			pro gly met gly thr phe ser val leu leu				
241/81																			271/91				
gta acc ggg aca acc ggc acc acg cct cgg																			tcg aga cgt atc gcg gca gcg ttg gcc ctg				
val thr gly thr thr gly thr thr pro arg																			ser arg arg ile ala ala ala leu ala leu				
301/101																			331/111				
tcg ttg ctg aca att acc gct ggc cgc cgc																			ata ttt gcc gcg ctg ccg cgg gcc gga tcc				
ser leu leu thr ile thr ala gly arg arg																			ile phe ala ala leu pro arg ala gly ser				
361/121																			391/131				
agg tcg acc tgc cag atc tca ccg cgc agc																			atc tac gcc gtt cgc tgc aaa ccg ccg act				
arg ser thr cys gln ile ser pro arg ser																			ile tyr ala val arg cys lys pro pro thr				
421/141																			451/151				
gcg acg gca ggc cca ctc tct tgg cat gcg																			tcc aat gct gcg acg tcc tcg gta gac aag				
ala thr ala gly pro leu ser trp his ala																			ser asn ala ala thr ser ser val asp lys				
481/161																			511/171				
ctc acg ctt ggc ttc atg ccg cag tcc tac																			cca tgt agt aac aga tag				
leu thr leu gly phe met pro gln ser tyr																			pro cys ser asn arg AMB				

FIGURE 34F

FIGURE 35A

1/1	31/11
GAC AGT CTG TCG GCA AGG AGG GAC GCA TGC	CAC TCT CCG ATC ATG AGC AGC GGA TGC TTG
asp ser leu ser ala arg arg asp ala cys	his ser pro ile met ser ser gly cys leu
61/21	91/31
ACC AGA TCG AGA GCG CTC TCT ACG CCG AAG	ATC CCA AGT TCG CAT CGA GTG TCC GTG GCG
thr arg ser arg ala leu ser thr pro lys	ile pro ser ser his arg val ser val ala
121/41	151/51
GGG GCT TCC GCG CAC CGA CCG CGC GGC GGC	GCC TGC AGG GCG CGG CGT TGT TCA TCA TCG
gly ala ser ala his arg pro arg gly gly	ala cys arg ala arg arg cys ser ser ser
181/61	211/71
GTC TGG GGA TGT TGG TTT CCG GCG TGG CGT	TCA AAG AGA CCA TGA TCG GAA GTT TCC CGA
val trp gly cys trp phe pro ala trp arg	ser lys arg pro OPA ser glu val ser arg
241/81	271/91
TAC TCA GCG TTT TCG GTT TTG TCG TGA TGT	TCG GTG GTG TGG TGT ATG CCA TCA CCG GTC
tyr ser ala phe ser val leu ser OPA cys	ser val val trp cys met pro ser pro val
301/101	331/111
CTC GGT TGT CCG GCA GGA TGG ATC GTG GCG	GAT CGG CTG CTG GGG CTT CGC GCC AGC GTC
leu gly cys pro ala gly trp ile val ala	asp arg leu leu gly leu arg ala ser val
361/121	391/131
GTA CCA AGG GGG CCG GGG GCT CAT TCA CCA	GCC GTA TGG AAG ATC
val pro arg gly pro gly ala his ser pro	ala val trp lys ile

SEQ ID No.35B

FIGURE 35B

1/1	31/11
ACA GTC TGT CGG CAA GGA GGG ACG CAT GCC	ACT CTC CGA TCA TGA GCA GCG GAT GCT TGA
thr val cys arg gln gly gly thr his ala	thr leu arg ser OPA ala ala asp ala OPA
61/21	91/31
CCA GAT CGA GAG CGC TCT CTA CGC CGA AGA	TCC CAA GTT CGC ATC GAG TGT CCG TGG CGG
pro asp arg glu arg ser leu arg arg arg	ser gln val arg ile glu cys pro trp arg
121/41	151/51
GGG CTT CCG CGC ACC GAC CGC GCG GCG GCG	CCT GCA GGG CGC GGC GTT GTT CAT CAT CGG
gly leu pro arg thr asp arg ala ala ala	pro ala gly arg gly val val his his arg
181/61	211/71
TCT GGG GAT GTT GGT TTC CGG CGT GGC GTT	CAA AGA GAC CAT GAT CGG AAG TTT CCC GAT
ser gly asp val gly phe arg arg gly val	gln arg asp his asp arg lys phe pro asp
241/81	271/91
ACT CAG CGT TTT CGG TTT TGT CGT GAT GTT	CGG TGG TGT GGT GTA TGC CAT CAC CGG TCC
thr gln arg phe arg phe cys arg asp val	arg trp cys gly val cys his his arg ser
301/101	331/111
TCG GTT GTC CGG CAG GAT GGA TCG TGG CGG	ATC GGC TGC TGG GGC TTC GCG CCA GCG TCG
ser val val arg gln asp gly ser trp arg	ile gly cys trp gly phe ala pro ala ser
361/121	391/131
TAC CAA GGG GGC CGG GGG CTC ATT CAC CAG	CCG TAT GGA AGA TC
tyr gln gly gly arg gly leu ile his gln	pro tyr gly arg

SEQ ID No.35C

FIGURE 35C

1/1											31/11										
atg cca ctc tcc gat cat gag cag cgg atg											ctt gac cag atc gag agc gct ctc tac gcc										
Met pro leu ser asp his glu gln arg met											leu asp gln ile glu ser ala leu tyr ala										
61/21											91/31										
gaa gat ccc aag ttc gca tcg agt gtc cgt											ggc ggg ggc ttc cgc gca ccg acc gcg cgg										
glu asp pro lys phe ala ser ser val arg											gly gly gly phe arg ala pro thr ala arg										
121/41											151/51										
cgg cgc ctg cag ggc gcg gcg ttg ttc atc											atc ggt ctg ggg atg ttg gtt tcc ggc gtg										
arg arg leu gln gly ala ala leu phe ile											ile gly leu gly met leu val ser gly val										
181/61											211/71										
gcg ttc aaa gag acc atg atc gga agt ttc											ccg ata ctc agc gtt ttc ggt ttt gtc gtg										
ala phe lys glu thr met ile gly ser phe											pro ile leu ser val phe gly phe val val										
241/81											271/91										
atg ttc ggt ggt gtg gtg tat gcc atc acc											ggt cct cgg ttg tcc ggc agg atg gat cgt										
met phe gly gly val val tyr ala ile thr											gly pro arg leu ser gly arg met asp arg										
301/101											331/111										
ggc gga tcg gct gct ggg gct tcg cgc cag											cgt cgt acc aag ggg gcc ggg ggc tca ttc										
gly gly ser ala ala gly ala ser arg gln											arg arg thr lys gly ala gly gly ser phe										
361/121											391/131										
acc agc cgt atg gaa gat cgg ttc cgg cgc											cgc ttc gac gag taa										
thr ser arg met glu asp arg phe arg arg											arg phe asp glu OCH										

FIGURE 35D

[illegible]

FIGURE 35F

1/1 31/11
 GAC CTG GGA CGA AGA CGA CGG CAG CAG CCG CAA TCA GAT CTA CCC GGT CCT GGT CAA CGT
 asp leu gly arg arg arg arg gln gln pro gln ser asp leu pro gly pro gly gln arg
 61/21 91/31
 CAA TGG ACA CCC GAC TAC GGT GCG CCT GCG CGG CTC GAC AAT GCG CGG TTC CTG TTG CCC
 gln trp thr pro asp tyr gly ala pro ala arg leu asp asn ala arg phe leu leu pro
 121/41 151/51
 GTG GTC GGA GTG CCA CCC GAC CAG GCC ACC GAC TTC GGC TCC GCT GTT GCA CCA GAA ACG
 val val gly val pro pro asp gln ala thr asp phe gly ser ala val ala pro glu thr
 181/61 211/71
 ACG GCG CCG GTC TGG ATC ACC ATG CTG TGG CCG CTG GCC GAC CGG CCC CGG TTG GCC CCC
 thr ala pro val trp ile thr met leu trp pro leu ala asp arg pro arg leu ala pro
 241/81 271/91
 GGG GCA CCC GGT GGC ACC GTT CCC GTC CGG CTG GTC GAC GAC GAC CTG GCA AAC TCG CTG
 gly ala pro gly gly thr val pro val arg leu val asp asp asp leu ala asn ser leu
 301/101 331/111
 GCC AAC GGC GGC CGG CTG GAC ATC CTC CTG TCG GCG GCC GAG TTC GCC ACC AAC CGG GAA
 ala asn gly gly arg leu asp ile leu leu ser ala ala glu phe ala thr asn arg glu
 361/121 391/131
 GTC GAC CCC GAC GGC GCC GTC GGC CGA GCG CTG TGC CTG GCC ATC GAC CCA GAT C
 val asp pro asp gly ala val gly arg ala leu cys leu ala ile asp pro asp

SEQ ID No.36A

FIGURE 36A

1/1 31/11
 ACC TGG GAC GAA GAC GAC GGC AGC AGC CGC AAT CAG ATC TAC CCG GTC CTG GTC AAC GTC
 thr trp asp glu asp asp gly ser ser arg asn gln ile tyr pro val leu val asn val
 61/21 91/31
 AAT GGA CAC CCG ACT ACG GTG CGC CTG CGC GGC TCG ACA ATG CGC GGT TCC TGT TGC CCG
 asn gly his pro thr thr val arg leu arg gly ser thr met arg gly ser cys cys pro
 121/41 151/51
 TGG TCG GAG TGC CAC CCG ACC AGG CCA CCG ACT TCG GCT CCG CTG TTG CAC CAG AAA CGA
 trp ser glu cys his pro thr arg pro pro thr ser ala pro leu leu his gln lys arg
 181/61 211/71
 CGG CGC CGG TCT GGA TCA CCA TGC TGT GGC CGC TGG CCG ACC GGC CCC GGT TGG CCC CCG
 arg arg arg ser gly ser pro cys cys gly arg trp pro thr gly pro gly trp pro pro
 241/81 271/91
 GGG CAC CCG GTG GCA CCG TTC CCG TCC GGC TGG TCG ACG ACG ACC TGG CAA ACT CGC TGG
 gly his pro val ala pro phe pro ser gly trp ser thr thr thr trp gln thr arg trp
 301/101 331/111
 CCA ACG GCG GCC GGC TGG ACA TCC TCC TGT CGG CGG CCG AGT TCG CCA CCA ACC GGG AAG
 pro thr ala ala gly trp thr ser ser cys arg arg pro ser ser pro pro thr gly lys
 361/121 391/131
 TCG ACC CCG ACG GCG CCG TCG GCC GAG CGC TGT GCC TGG CCA TCG ACC CAG ATC
 ser thr pro thr ala pro ser ala glu arg cys ala trp pro ser thr gln ile

SEQ ID No.36B

FIGURE 36B

110/185

1/1	31/11
CCT GGG ACG AAG ACG ACG GCA GCA GCC GCA	ATC AGA TCT ACC CGG TCC TGG TCA ACG TCA
pro gly thr lys thr thr ala ala ala ala	ile arg ser thr arg ser trp ser thr ser
61/21	91/31
ATG GAC ACC CGA CTA CGG TGC GCC TGC GCG	GCT CGA CAA TGC GCG GTT CCT GTT GCC CGT
met asp thr arg leu arg cys ala cys ala	ala arg gln cys ala val pro val ala arg
121/41	151/51
GGT CGG AGT GCC ACC CGA CCA GGC CAC CGA	CTT CGG CTC CGC TGT TGC ACC AGA AAC GAC
gly arg ser ala thr arg pro gly his arg	leu arg leu arg cys cys thr arg asn asp
181/61	211/71
GGC GCC GGT CTG GAT CAC CAT GCT GTG GCC	GCT GGC CGA CCG GCC CCG GTT GGC CCC CGG
gly ala gly leu asp his his ala val ala	ala gly arg pro ala pro val gly pro arg
241/81	271/91
GGC ACC CGG TGG CAC CGT TCC CGT CCG GCT	GGT CGA CGA CGA CCT GGC AAA CTC GCT GGC
gly thr arg trp his arg ser arg pro ala	gly arg arg arg pro gly lys leu ala gly
301/101	331/111
CAA CGG CGG CCG GCT GGA CAT CCT CCT GTC	GGC GGC CGA GTT CGC CAC CAA CCG GGA AGT
gln arg arg pro ala gly his pro pro val	gly gly arg val arg his gln pro gly ser
361/121	391/131
CGA CCC CGA CGG CGC CGT CGG CCG AGC GCT	GTG CCT GGC CAT CGA CCC AGA TC
arg pro arg arg arg arg arg pro ser ala	val pro gly his arg pro arg

SEQ ID No.36 C

FIGURE 36C

Coding sequence Rv3909 predicted by Cole et al., 1998 (Nature 393 537-544) containing Seq 36A

1/1	31/11
GTG ACC GCA CTG CAA CTC GGC TGG GCC GCT	TTG GCG CGC GTC ACC TCA GCG ATC GGC GTC
met thr ala leu gln leu gly trp ala ala	leu ala arg val thr ser ala ile gly val
61/21	91/31
GTG GCC GGC CTC GGG ATG GCG CTC ACG GTA	CCG TCG GCG GCA CCG CAC GCG CTC GCA GGC
val ala gly leu gly met ala leu thr val	pro ser ala ala pro his ala leu ala gly
121/41	151/51
GAG CCC AGC CCG ACG CCT TTT GTC CAG GTC	CGC ATC GAT CAG GTG ACC CCG GAC GTG GTG
glu pro ser pro thr pro phe val gln val	arg ile asp gln val thr pro asp val val
181/61	211/71
ACC ACT TCC AGC GAA CCC CAT GTC ACC GTC	AGC GGA ACG GTG ACC AAT ACC GGT GAC CGC
thr thr ser ser glu pro his val thr val	ser gly thr val thr asn thr gly asp arg
241/81	271/91
CCA GTC CGC GAT GTG ATG GTC CGG CTT GAG	CAC GCC GCC GCG GTC ACG TCG TCA ACG GCG
pro val arg asp val met val arg leu glu	his ala ala ala val thr ser ser thr ala
301/101	331/111
TTA CGC ACC TCG CTC GAC GGC GGC ACC GAC	CAG TAC CAG CCG GCC GCG GAC TTC CTC ACG
leu arg thr ser leu asp gly gly thr asp	gln tyr gln pro ala ala asp phe leu thr

SEQ ID No.36D

FIGURE 36D

361/121
 GTC GCC CCC GAA CTA GAC CGC GGG CAA GAG
 val ala pro glu leu asp arg gly gln glu
 421/141
 TCG CTG ACC AGG CCG TCG TTG GCC GTC AAC
 ser leu thr arg pro ser leu ala val asn
 481/161
 GTC AAT GGG ACA CCC GAC TAC GGT GCG CCT
 val asn gly thr pro asp tyr gly ala pro
 541/181
 CCC GTG GTC GGA GTG CCA CCC GAC CAG GCC
 pro val val gly val pro pro asp gln ala
 601/201
 ACG ACG GCG CCG GTC TGG ATC ACC ATG CTG
 thr thr ala pro val trp ile thr met leu
 661/221
 CCC GGG GCA CCC GGT GGC ACC GTT CCC GTC
 pro gly ala pro gly gly thr val pro val
 721/241
 CTG GCC AAC GGC GGC CCG CTG GAC ATC CTC
 leu ala asn gly gly arg leu asp ile leu
 781/261
 GAA GTC GAC CCC GAC GGC GCC GTC GGC CGA
 glu val asp pro asp gly ala val gly arg
 841/281
 CTC ATC ACC GTC AAT GCG ATG ACC GGC GGC
 leu ile thr val asn ala met thr gly gly
 901/301
 GCT CAA CTA CCG GGC ACC CCG ACC CAC CCG
 ala gln leu pro gly thr pro thr his pro
 961/321
 CTG GAT CGA TTG CCG ACG CTA GTC CAC CGG
 leu asp arg leu arg thr leu val his arg
 1021/341
 GCC GAC CTG GAT GCT TTG CAG CGG GTT AAT
 ala asp leu asp ala leu gln arg val asn
 1081/361
 AGC CCC GCC GAC ATC GTC GAC CGC ATC CTG
 ser pro ala asp ile val asp arg ile leu
 1141/381
 CTG CCC GAC GGC CCG TTG ACC GGC CGG GCG
 leu pro asp gly pro leu thr gly arg ala
 1201/401
 GTT GCC GTC GCG GCC GCC GAT TTT AGC CCC
 val ala val ala ala asp phe ser pro
 1261/421
 TCC GCG CTC TTA CCC GCT ACC GCG CCC CGG
 ser ala leu leu pro ala thr ala pro arg
 1321/441
 TTT GAT CCC GCG GTC GGG GCC GCG CTG GCC
 phe asp pro ala val gly ala ala leu ala
 1381/461
 TAT CTA GAT CCC TCG TTG TTC GTT CGG ATC
 tyr leu asp pro ser leu phe val arg ile
 391/131
 GCC GGC TTT ACC CTC TCG GCC CCG CTG CGC
 ala gly phe thr leu ser ala pro leu arg
 451/151
 CAG CCC GGG ATC TAC CCG GTC CTG GTC AAC
 gln pro gly ile tyr pro val leu val asn
 511/171
 GCG CGG CTC GAC AAT GCG CGG TTC CTG TTG
 ala arg leu asp asn ala arg phe leu leu
 571/191
 ACC GAC TTC GGC TCC GCT GTT GCA CCA GAA
 thr asp phe gly ser ala val ala pro glu
 631/211
 TGG CCG CTG GCC GAC CGG CCC CGG TTG GCC
 trp pro leu ala asp arg pro arg leu ala
 691/231
 CCG CTG GTC GAC GAC GAC CTG GCA AAC TCG
 arg leu val asp asp asp leu ala asn ser
 751/251
 CTG TCG GCG GCC GAG TTC GCC ACC AAC CGG
 leu ser ala ala glu phe ala thr asn arg
 811/271
 GCG CTG TGC CTG GCC ATC GAC CCA GAT CTA
 ala leu cys leu ala ile asp pro asp leu
 871/291
 TAC GTC GTG TCC GAC TCG CCC GAC GGG GCC
 tyr val val ser asp ser pro asp gly ala
 931/311
 GGC ACC GGC CAG GCC GCC GCA TCC AGC TGG
 gly thr gly gln ala ala ala ser ser trp
 991/331
 ACA TGC GTG ACG CCG CTG CCT TTT GCC CAA
 thr cys val thr pro leu pro phe ala gln
 1051/351
 GAT CCG AGG CTG AGC GCG ATC GCA ACC ATC
 asp pro arg leu ser ala ile ala thr ile
 1111/371
 GAT GTC AGC TCC ACC CGC GGC GCA ACC GTG
 asp val ser ser thr arg gly ala thr val
 1171/391
 ATC AAC TTG CTC AGC ACC CAC GGC AAC ACG
 ile asn leu leu ser thr his gly asn thr
 1231/411
 GAG GAA CAG CAG GGT TCG TCC CAG ATC GGC
 glu glu gln gln gly ser ser gln ile gly
 1291/431
 CCG TTG TCC CCG CGG GTG GTA GCG GCG CCG
 arg leu ser pro arg val val ala ala pro
 1351/451
 GCC GCG GGA ACA AAC CCG ACC GTT CCT ACC
 ala ala gly thr asn pro thr val pro thr
 1411/471
 GCG CAT GAA TCG ATC ACC GCG CGC CGC CAG
 ala his glu ser ile thr ala arg arg gln

SEQ ID No.36D(continued 1)

FIGURE 36D (continued 1)

REPLACEMENT SHEET (RULE 26)

1441/481
 GAC GCC TTG GGC GCA ATG CTG TGG CGC AGC
 asp ala leu gly ala met leu trp arg ser
 1501/501
 ATC CTG GTG CCG CCG GCG TCG TGG AGC CTG
 ile leu val pro pro ala ser trp ser leu
 1561/521
 GCG CTG GCC ACC GCC ATC CGG TCT GGC CTG
 ala leu ala thr ala ile arg ser gly leu
 1621/541
 GCT GAC GCC GCG GCC CGC ACC GAG CCA CCG
 ala asp ala ala ala arg thr glu pro pro
 1681/561
 GGC CGG TTC AAT GAC GAC ATC ACC ACG CAG
 gly arg phe asn asp asp ile thr thr gln
 1741/581
 CTG ACC TCG GCG TTG ACC ATC GAT GAC CGC
 leu thr ser ala leu thr ile asp asp arg
 1801/601
 CCA CTA CGC GAG GAC ATG TTG CGC GCG CTG
 pro leu arg glu asp met leu arg ala leu
 1861/621
 GGG CTG GCC CAG CAG CGG CTG GCC GTC GTT
 gly leu ala gln gln arg leu ala val val
 1921/641
 GTG ACC ATC GTC AAC CCG GGC GGC TCC TAC
 val thr ile val asn pro gly gly ser tyr
 1981/661
 TTG GCG CTG CAT AAT GGC CTC GCC GTG CCA
 leu ala leu his asn gly leu ala val pro
 2041/681
 CCC GGG ATG ACG GTG GCC GAT GTC GGT CAG
 pro gly met thr val ala asp val gly gln
 2101/701
 CGA GTA CCA ATC GAG GTG AAC TTC ACA CAG
 arg val pro ile glu val asn phe thr gln
 2161/721
 CCC GAC GGC GTC GCG CTG GGT GAA CCG GTG
 pro asp gly val ala leu gly glu pro val
 2221/741
 AAG GTG TTG TTC GCG ATC ACG CTA TCC GCT
 lys val leu phe ala ile thr leu ser ala
 2281/761
 CGC CTT TGG CAC CGG TTC CGT GGC CAG CCT
 arg leu trp his arg phe arg gly gln pro
 2341/781
 CCT ACC GGC AAA CAC GCC CCG CAG CGC CGT
 pro thr gly lys his ala pro gln arg arg
 2401/801
 CGG GTA TGA
 arg val OPA

1471/491
 TTG GAG CCG AAT GCC GCG CCC CGT ACC CAA
 leu glu pro asn ala ala pro arg thr gln
 1531/511
 GCC AGC GAC GAC GCG CAG GTC ATC CTG ACC
 ala ser asp asp ala gln val ile leu thr
 1591/531
 GCC GTG CCG CGA CCA CTA CCG GCG GTG ATC
 ala val pro arg pro leu pro ala val ile
 1651/551
 GAA CCC CCG GGC GCT TAC AGC GCC GCT CGC
 glu pro pro gly ala tyr ser ala ala arg
 1711/571
 ATC GGC GGG CAG GTT GCC CGG CTA TGG AAG
 ile gly gly gln val ala arg leu trp lys
 1771/591
 ACC GGG CTG ACC GGC GTG CAG TAC ACC GCA
 thr gly leu thr gly val gln tyr thr ala
 1831/611
 AGC CAA TCG CTA CCA CCC GAT ACC CGC AAC
 ser gln ser leu pro pro asp thr arg asn
 1891/631
 GGA AAG ACG ATC GAC GAT CTT TTC GGC GCG
 gly lys thr ile asp asp leu phe gly ala
 1951/651
 ACT CTG GCC ACC GAG CAC AGT CCG CTG CCG
 thr leu ala thr glu his ser pro leu pro
 2011/671
 ATC CGG GTC CGG CTA CAG GTC GAT GCT CCG
 ile arg val arg leu gln val asp ala pro
 2071/691
 ATC GAG CTA CCG CCC GGG TAC CTG CCG CTA
 ile glu leu pro pro gly tyr leu pro leu
 2131/711
 CGG GTT GCC GTC GAC GTG TCG CTG CGG ACC
 arg val ala val asp val ser leu arg thr
 2191/731
 CGG TTG TCG GTG CAC TCC AAC GCC TAC GGC
 arg leu ser val his ser asn ala tyr gly
 2251/751
 GCG GCC GTG CTG GTA ACG CTG GCG GGC CGG
 ala ala val leu val thr leu ala gly arg
 2311/771
 GAT CGC GCC GAC CTG GAT CGC CCC GAC CTG
 asp arg ala asp leu asp arg pro asp leu
 2371/791
 GCC GTA GCC AGT CGG GAT GAC GAA AAG CAC
 ala val ala ser arg asp asp glu lys his

SEQ ID No.36D (continued 2)

FIGURE 36D (continued 2)

ORF according to Cole et al., 1998 (Nature 393 537-544) and containing Rv 3909.

1/1	31/11
TGA CTC AGC ACC GGG TCA GCA CAA CGG TCC	CGG GCC GGG GCC GTG ACC GCA CTG CAA CTC
OPA leu ser thr gly ser ala gln arg ser	arg ala gly ala val thr ala leu gln leu
61/21	91/31
GGC TGG GCC GCT TTG GCG CGC GTC ACC TCA	GCG ATC GGC GTC GTG GCC GGC CTC GGG ATG
gly trp ala ala leu ala arg val thr ser	ala ile gly val val ala gly leu gly met
121/41	151/51
GCG CTC ACG GTA CCG TCG GCG GCA CCG CAC	GCG CTC GCA GGC GAG CCC AGC CCG ACG CCT
ala leu thr val pro ser ala ala pro his	ala leu ala gly glu pro ser pro thr pro
181/61	211/71
TTT GTC CAG GTC CGC ATC GAT CAG GTG ACC	CCG GAC GTG GTG ACC ACT TCC AGC GAA CCC
phe val gln val arg ile asp gln val thr	pro asp val val thr thr ser ser glu pro
241/81	271/91
CAT GTC ACC GTC AGC GGA ACG GTG ACC AAT	ACC GGT GAC CGC CCA GTC CGC GAT GTG ATG
his val thr val ser gly thr val thr asn	thr gly asp arg pro val arg asp val met
301/101	331/111
GTC CGG CTT GAG CAC GCC GCC GCG GTC ACG	TCG TCA ACG GCG TTA CGC ACC TCG CTC GAC
val arg leu glu his ala ala ala val thr	ser ser thr ala leu arg thr ser leu asp
361/121	391/131
GGC GGC ACC GAC CAG TAC CAG CCG GCC GCG	GAC TTC CTC ACG GTC GCC CCC GAA CTA GAC
gly gly thr asp gln tyr gln pro ala ala	asp phe leu thr val ala pro glu leu asp
421/141	451/151
CGC GGG CAA GAG GCC GGC TTT ACC CTC TCG	GCC CCG CTG CGC TCG CTG ACC AGG CCG TCG
arg gly gln glu ala gly phe thr leu ser	ala pro leu arg ser leu thr arg pro ser
481/161	511/171
TTG GCC GTC AAC CAG CCC GGG ATC TAC CCG	GTC CTG GTC AAC GTC AAT GGG ACA CCC GAC
leu ala val asn gln pro gly ile tyr pro	val leu val asn val asn gly thr pro asp
541/181	571/191
TAC GGT GCG CCT GCG CGG CTC GAC AAT GCG	CGG TTC CTG TTG CCC GTG GTC GGA GTG CCA
tyr gly ala pro ala arg leu asp asn ala	arg phe leu leu pro val val gly val pro
601/201	631/211
CCC GAC CAG GCC ACC GAC TTC GGC TCC GCT	GTT GCA CCA GAA ACG ACG GCG CCG GTC TGG
pro asp gln ala thr asp phe gly ser ala	val ala pro glu thr thr ala pro val trp
661/221	691/231
ATC ACC ATG CTG TGG CCG CTG GCC GAC CGG	CCC CGG TTG GCC CCC GGG GCA CCC GGT GGC
ile thr met leu trp pro leu ala asp arg	pro arg leu ala pro gly ala pro gly gly
721/241	751/251
ACC GTT CCC GTC CGG CTG GTC GAC GAC GAC	CTG GCA AAC TCG CTG GCC AAC GGC GGC CGG
thr val pro val arg leu val asp asp asp	leu ala asn ser leu ala asn gly gly arg
781/261	811/271
CTG GAC ATC CTC CTG TCG GCG GCC GAG TTC	GCC ACC AAC CGG GAA GTC GAC CCC GAC GGC
leu asp ile leu leu ser ala ala glu phe	ala thr asn arg glu val asp pro asp gly
841/281	871/291
GCC GTC GGC CGA GCG CTG TGC CTG GCC ATC	GAC CCA GAT CTA CTC ATC ACC GTC AAT GCG
ala val gly arg ala leu cys leu ala ile	asp pro asp leu leu ile thr val asn ala
901/301	931/311
ATG ACC GGC GGC TAC GTC GTG TCC GAC TCG	CCC GAC GGG GCC GCT CAA CTA CCG GGC ACC
met thr gly gly tyr val val ser asp ser	pro asp gly ala ala gln leu pro gly thr
961/321	991/331
CCG ACC CAC CCG GGC ACC GGC CAG GCC GCC	GCA TCC AGC TGG CTG GAT CGA TTG CGG ACG
pro thr his pro gly thr gly gln ala ala	ala ser ser trp leu asp arg leu arg thr

SEQ ID No.36F

FIGURE 36F

REPLACEMENT SHEET (RULE 26)

1021/341	CTA GTC CAC CGG ACA TGC GTG ACG CCG CTG	1051/351	CCT TTT GCC CAA GCC GAC CTG GAT GCT TTG
leu val his arg thr cys val thr pro leu		pro phe ala gln ala asp leu asp ala leu	
1081/361	CAG CGG GTT AAT GAT CCG AGG CTG AGC GCG	1111/371	ATC GCA ACC ATC AGC CCC GCC GAC ATC GTC
gln arg val asn asp pro arg leu ser ala		ile ala thr ile ser pro ala asp ile val	
1141/381	GAC CGC ATC CTG GAT GTC AGC TCC ACC CGC	1171/391	GGC GCA ACC GTG CTG CCC GAC GGC CCG TTG
asp arg ile leu asp val ser ser thr arg		gly ala thr val leu pro asp gly pro leu	
1201/401	ACC GGC CGG GCG ATC AAC TTG CTC AGC ACC	1231/411	CAC GGC AAC ACG GTT GCC GTC GCG GCC GCC
thr gly arg ala ile asn leu leu ser thr		his gly asn thr val ala val ala ala ala	
1261/421	GAT TTT AGC CCC GAG GAA CAG CAG GGT TCG	1291/431	TCC CAG ATC GGC TCC GCG CTC TTA CCC GCT
asp phe ser pro glu glu gln gln gly ser		ser gln ile gly ser ala leu leu pro ala	
1321/441	ACC GCG CCC CGG CGG TTG TCC CCG CGG GTG	1351/451	GTA GCG GCG CCG TTT GAT CCC GCG GTC GGG
thr ala pro arg arg leu ser pro arg val		val ala ala pro phe asp pro ala val gly	
1381/461	GCC GCG CTG GCC GCC GCG GGA ACA AAC CCG	1411/471	ACC GTT CCT ACC TAT CTA GAT CCC TCG TTG
ala ala leu ala ala ala gly thr asn pro		thr val pro thr tyr leu asp pro ser leu	
1441/481	TTC GTT CGG ATC GCG CAT GAA TCG ATC ACC	1471/491	GCG CGC CGC CAG GAC GCC TTG GGC GCA ATG
phe val arg ile ala his glu ser ile thr		ala arg arg gln asp ala leu gly ala met	
1501/501	CTG TGG CGC AGC TTG GAG CCG AAT GCC GCG	1531/511	CCC CGT ACC CAA ATC CTG GTG CCG CCG GCG
leu trp arg ser leu glu pro asn ala ala		pro arg thr gln ile leu val pro pro ala	
1561/521	TCG TGG AGC CTG GCC AGC GAC GAC GCG CAG	1591/531	GTC ATC CTG ACC GCG CTG GCC ACC GCC ATC
ser trp ser leu ala ser asp asp ala gln		val ile leu thr ala leu ala thr ala ile	
1621/541	CGG TCT GGC CTG GCC GTG CCG CGA CCA CTA	1651/551	CCG GCG GTG ATC GCT GAC GCC GCG GCC CGC
arg ser gly leu ala val pro arg pro leu		pro ala val ile ala asp ala ala ala arg	
1681/561	ACC GAG CCA CCG GAA CCC CCG GGC GCT TAC	1711/571	AGC GCC GCT CGC GGC CGG TTC AAT GAC GAC
thr glu pro pro glu pro pro gly ala tyr		ser ala ala arg gly arg phe asn asp asp	
1741/581	ATC ACC ACG CAG ATC GGC GGG CAG GTT GCC	1771/591	CGG CTA TGG AAG CTG ACC TCG GCG TTG ACC
ile thr thr gln ile gly gly gln val ala		arg leu trp lys leu thr ser ala leu thr	
1801/601	ATC GAT GAC CGC ACC GGG CTG ACC GGC GTG	1831/611	CAG TAC ACC GCA CCA CTA CGC GAG GAC ATG
ile asp asp arg thr gly leu thr gly val		gln tyr thr ala pro leu arg glu asp met	
1861/621	TTG CGC GCG CTG AGC CAA TCG CTA CCA CCC	1891/631	GAT ACC CGC AAC GGG CTG GCC CAG CAG CGG
leu arg ala leu ser gln ser leu pro pro		asp thr arg asn gly leu ala gln gln arg	
1921/641	CTG GCC GTC GTT GGA AAG ACG ATC GAC GAT	1951/651	CTT TTC GGC GCG GTG ACC ATC GTC AAC CCG
leu ala val val gly lys thr ile asp asp		leu phe gly ala val thr ile val asn pro	
1981/661	GGC GGC TCC TAC ACT CTG GCC ACC GAG CAC	2011/671	AGT CCG CTG CCG TTG GCG CTG CAT AAT GGC
gly gly ser tyr thr leu ala thr glu his		ser pro leu pro leu ala leu his asn gly	

SEQ ID 36F (continued 1)

FIGURE 36F (continued 1)

2041/681 2071/691
 CTC GCC GTG CCA ATC CGG GTC CGG CTA CAG GTC GAT GCT CCG CCC GGG ATG ACG GTG GCC
 leu ala val pro ile arg val arg leu gln val asp ala pro pro gly met thr val ala
 2101/701 2131/711
 GAT GTC GGT CAG ATC GAG CTA CCG CCC GGG TAC CTG CCG CTA CGA GTA CCA ATC GAG GTG
 asp val gly gln ile glu leu pro pro gly tyr leu pro leu arg val pro ile glu val
 2161/721 2191/731
 AAC TTC ACA CAG CGG GTT GCC GTC GAC GTG TCG CTG CGG ACC CCC GAC GGC GTC GCG CTG
 asn phe thr gln arg val ala val asp val ser leu arg thr pro asp gly val ala leu
 2221/741 2251/751
 GGT GAA CCG GTG CGG TTG TCG GTG CAC TCC AAC GCC TAC GGC AAG GTG TTG TTC GCG ATC
 gly glu pro val arg leu ser val his ser asn ala tyr gly lys val leu phe ala ile
 2281/761 2311/771
 ACG CTA TCC GCT GCG GCC GTG CTG GTA ACG CTG GCG GGC CGG CGC CTT TGG CAC CGG TTC
 thr leu ser ala ala ala val leu val thr leu ala gly arg arg leu trp his arg phe
 2341/781 2371/791
 CGT GGC CAG CCT GAT CGC GCC GAC CTG GAT CGC CCC GAC CTG CCT ACC GGC AAA CAC GCC
 arg gly gln pro asp arg ala asp leu asp arg pro asp leu pro thr gly lys his ala
 2401/801 2431/811
 CCG CAG CGC CGT GCC GTA GCC AGT CGG GAT GAC GAA AAG CAC CGG GTA TGA
 pro gln arg arg ala val ala ser arg asp asp glu lys his arg val OPA

SEQ ID 36F (continued 2)

FIGURE 36F (continued 2)

1/1 31/11
 ATC CGC GCG TTG GCG TCG CAT CCG AAC ATC GTC GGA GTC AAG GAC GCC AAA GCC GAC CTG
 ile arg ala leu ala ser his pro asn ile val gly val lys asp ala lys ala asp leu
 61/21 91/31
 CAC AGC GGC GCC CAA ATC ATG GCC GAC ACC GGA CTG GCC TAC TAT TCC GGC GAC GAC GCG
 his ser gly ala gln ile met ala asp thr gly leu ala tyr tyr ser gly asp asp ala
 121/41 151/51
 CTC AAC CTG CCC TGG CTG GCC ATG GGC GCC ACG GGC TTC ATC AGC GTG ATT GCC CAC CTG
 leu asn leu pro trp leu ala met gly ala thr gly phe ile ser val ile ala his leu
 181/61 211/71
 GCA GCC GGG CAG CTT CGA GAG TTG TTG TCC GCC TTC GGT TCT GGG GAT ATC GCC ACC GCC
 ala ala gly gln leu arg glu leu leu ser ala phe gly ser gly asp ile ala thr ala
 241/81
 CGC AAG ATC
 arg lys ile

SEQ ID No.37A

FIGURE 37A


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1/1                               31/11
GAT CCG CGC GTT GGC GTC GCA TCC GAA CAT CGT CGG AGT CAA GGA CGC CAA AGC CGA CCT
asp pro arg val gly val ala ser glu his arg arg ser gln gly arg gln ser arg pro
61/21                               91/31
GCA CAG CGG CGC CCA AAT CAT GGC CGA CAC CGG ACT GGC CTA CTA TTC CGG CGA CGA CGC
ala gln arg arg pro asn his gly arg his arg thr gly leu leu phe arg arg arg arg
121/41                               151/51
GCT CAA CCT GCC CTG GCT GGC CAT GGG CGC CAC GGG CTT CAT CAG CGT GAT TGC CCA CCT
ala gln pro ala leu ala gly his gly arg his gly leu his gln arg asp cys pro pro
181/61                               211/71
GGC AGC CGG GCA GCT TCG AGA GTT GTT GTC CGC CTT CGG TTC TGG GGA TAT CGC CAC CGC
gly ser arg ala ala ser arg val val val arg leu arg phe trp gly tyr arg his arg
241/81
CCG CAA GAT C
pro gln asp

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SEQ ID No.37B

FIGURE 37B

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1/1                               31/11
TCC GCG CGT TGG CGT CGC ATC CGA ACA TCG TCG GAG TCA AGG ACG CCA AAG CCG ACC TGC
ser ala arg trp arg arg ile arg thr ser ser glu ser arg thr pro lys pro thr cys
61/21                               91/31
ACA GCG GCG CCC AAA TCA TGG CCG ACA CCG GAC TGG CCT ACT ATT CCG GCG ACG ACG CGC
thr ala ala pro lys ser trp pro thr pro asp trp pro thr ile pro ala thr thr arg
121/41                               151/51
TCA ACC TGC CCT GGC TGG CCA TGG GCG CCA CGG GCT TCA TCA GCG TGA TTG CCC ACC TGG
ser thr cys pro gly trp pro trp ala pro arg ala ser ser ala OPA leu pro thr trp
181/61                               211/71
CAG CCG GGC AGC TTC GAG AGT TGT TGT CCG CCT TCG GTT CTG GGG ATA TCG CCA CCG CCC
gln pro gly ser phe glu ser cys cys pro pro ser val leu gly ile ser pro pro pro
241/81
GCA AGA TC
ala arg

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SEQ ID No.37C

FIGURE 37C

117/185

Coding sequence Rv2753c predicted by Cole et al., 1998 (Nature 393 537-544) containing Seq 37A

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1/1                                     31/11
GTG ACC ACC GTC GGA TTC GAC GTC GCA GCG CGC CTA GGA ACC CTG CTG ACC GCG ATG GTG
val thr thr val gly phe asp val ala ala arg leu gly thr leu leu thr ala met val
61/21                                     91/31
ACA CCG TTT AGC GGC GAT GGC TCC CTG GAC ACC GCC ACC GCG GCG CGG CTG GCC AAC CAC
thr pro phe ser gly asp gly ser leu asp thr ala thr ala ala arg leu ala asn his
121/41                                     151/51
CTG GTC GAT CAG GGG TGC GAC GGT CTG GTG GTC TCG GGC ACC ACC GGC GAG TCG CCG ACC
leu val asp gln gly cys asp gly leu val val ser gly thr thr gly glu ser pro thr
181/61                                     211/71
ACC ACC GAC GGG GAG AAA ATC GAG CTG CTG CGG GCC GTC TTG GAA GCG GTG GGG GAC CGG
thr thr asp gly glu lys ile glu leu leu arg ala val leu glu ala val gly asp arg
241/81                                     271/91
GCC CGT GTT ATC GCC GGT GCC GGC ACC TAT GAC ACC GCG CAC AGC ATC CGG CTG GCC AAG
ala arg val ile ala gly ala gly thr tyr asp thr ala his ser ile arg leu ala lys
301/101                                    331/111
GCT TGT GCG GCC GAG GGT GCG CAC GGG CTG CTG GTG GTC ACG CCC TAC TAT TCC AAG CCG
ala cys ala ala glu gly ala his gly leu leu val val thr pro tyr tyr ser lys pro
361/121                                    391/131
CCG CAG CGG GGG CTG CAA GCC CAT TTC ACC GCC GTC GCC GAC GCG ACC GAG CTG CCG ATG
pro gln arg gly leu gln ala his phe thr ala val ala asp ala thr glu leu pro met
421/141                                    451/151
CTG CTC TAT GAC ATC CCG GGG CGG TCG GCG GTG CCG ATC GAG CCC GAC ACG ATC CGC GCG
leu leu tyr asp ile pro gly arg ser ala val pro ile glu pro asp thr ile arg ala
481/161                                    511/171
TTG GCG TCG CAT CCG AAC ATC GTC GGA GTC AAG GAC GCC AAA GCC GAC CTG CAC AGC GGC
leu ala ser his pro asn ile val gly val lys asp ala lys ala asp leu his ser gly
541/181                                    571/191
GCC CAA ATC ATG GCC GAC ACC GGA CTG GCC TAC TAT TCC GGC GAC GAC GCG CTC AAC CTG
ala gln ile met ala asp thr gly leu ala tyr tyr ser gly asp asp ala leu asn leu
601/201                                    631/211
CCC TGG CTG GCC ATG GGC GCC ACG GGC TTC ATC AGC GTG ATT GCC CAC CTG GCA GCC GGG
pro trp leu ala met gly ala thr gly phe ile ser val ile ala his leu ala ala gly
661/221                                    691/231
CAG CTT CGA GAG TTG TTG TCC GCC TTC GGT TCT GGG GAT ATC GCC ACC GCC CGC AAG ATC
gln leu arg glu leu leu ser ala phe gly ser gly asp ile ala thr ala arg lys ile
721/241                                    751/251
AAC ATT GCG GTC GCC CCG CTG TGC AAC GCG ATG AGC CGC CTG GGT GGG GTG ACG TTG TCC
asn ile ala val ala pro leu cys asn ala met ser arg leu gly gly val thr leu ser
781/261                                    811/271
AAG GCG GGC TTG CGG CTG CAG GGC ATC GAC GTC GGT GAT CCC CGG CTG CCC CAG GTG GCC
lys ala gly leu arg leu gln gly ile asp val gly asp pro arg leu pro gln val ala
841/281                                    871/291
GCG ACA CCG GAG CAG ATC GAC GCG TTG GCC GCC GAC ATG CGC GCG GCC TCG GTG CTT CGG
ala thr pro glu gln ile asp ala leu ala ala asp met arg ala ala ser val leu arg
901/301
TGA
OPA

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SEQ ID No.37D

FIGURE 37D

ORF according to Cole et al., 1998 (Nature 393 537-544) containing Rv2753c

1/1	31/11
TAA GGT GAG CGC CGT GGC CGA GAC CGC GCC	GCT GCG CGT GCA ACT GAT CGC CAA GAC CGA
OCH gly glu arg arg gly arg asp arg ala	ala ala arg ala thr asp arg gln asp arg
61/21	91/31
CTT CTT GGC CCC ACC CGA CGT GCC CTG GAC	CAC CGA CGC CGA CGG CGG ACC CGC GCT GGT
leu leu gly pro thr arg arg ala leu asp	his arg arg arg arg arg thr arg ala gly
121/41	151/51
CGA GTT CGC CGG CCG GGC CTG CTA TCA GAG	CTG GTC CAA GCC CAA TCC CAA GAC CGC CAC
arg val arg arg pro gly leu leu ser glu	leu val gln ala gln ser gln asp arg his
181/61	211/71
CAA CGC CGG CTA CCT CCG GCA CAT CAT CGA	CGT CCG ACA TTT CTC GGT GCT AGA GCA TGC
gln arg arg leu pro pro ala his his arg	arg arg thr phe leu gly ala arg ala cys
241/81	271/91
CAG CGT GTC GTT CTA CAT CAC CGG GAT CTC	GCG ATC GTG CAC CCA CGA GCT GAT CCG CCA
gln arg val val leu his his arg asp leu	ala ile val his pro arg ala asp pro pro
301/101	331/111
CCG GCA TTT CTC CTA CTC GCA GCT CTC CCA	GCG CTA CGT ACC CGA GAA GGA CTC GCG GGT
pro ala phe leu leu leu ala ala leu pro	ala leu arg thr arg glu gly leu ala gly
361/121	391/131
CGT CGT GCC GCC CGG CAT GGA GGA CGA CGC	CGA CCT GCG CCA CAT CCT GAC CGA GGC CGC
arg arg ala ala arg his gly gly arg arg	arg pro ala pro his pro asp arg gly arg
421/141	451/151
CGA CGC CGC CCG CGC CAC CTA CAG CGA GCT	GCT GGC CAA GCT GGA AGC CAA GTT CGC CGA
arg arg arg pro arg his leu gln arg ala	ala gly gln ala gly ser gln val arg arg
481/161	511/171
CCA ACC CAA CGC GAT CCT GCG CCG CAA GCA	GGC CCG CCA AGC CGC CCG CGC GGT GCT GCC
pro thr gln arg asp pro ala pro gln ala	gly pro pro ser arg pro arg gly ala ala
541/181	571/191
CAA CGC CAC CGA AAC CCG CAT CGT GGT GAC	CGG CAA CTA CCG GGC CTG GCG GCA CTT CAT
gln arg his arg asn pro his arg gly asp	arg gln leu pro gly leu ala ala leu his
601/201	631/211
CGC AAT GCG GGC CAG CGA GCA CGC CGA CGT	GGA AAT CCG GCG ACT GGC CAT CGA ATG CCT
arg asn ala gly gln arg ala arg arg arg	gly asn pro ala thr gly his arg met pro
661/221	691/231
GCG CCA GCT CGC CGC CGT GGC CCC CGC GGT	GTT CGC CGA CTT CGA GGT GAC CAC CCT GGC
ala pro ala arg arg arg gly pro arg gly	val arg arg leu arg gly asp his pro gly
721/241	751/251
CGA CGG CAC CGA GGT GGC GAC CAG CCC GTT	GGC GAC CGA AGC CTG AGG CGG CGT GTC GCT
arg arg his arg gly gly asp gln pro val	gly asp arg ser leu arg arg arg val ala
781/261	811/271
GGA CAA ACA CGC GCG CTC GCG GCC GGG ATA	AAG CGC CAG GTA ACC TTG GGA GCC GTG ACC
gly gln thr arg ala leu ala ala gly ile	lys arg gln val thr leu gly ala val thr
841/281	871/291
ACC GTC GGA TTC GAC GTC GCA GCG CGC CTA	GGA ACC CTG CTG ACC GCG ATG GTG ACA CCG
thr val gly phe asp val ala ala arg leu	gly thr leu leu thr ala met val thr pro
901/301	931/311
TTT AGC GGC GAT GGC TCC CTG GAC ACC GCC	ACC GCG GCG CGG CTG GCC AAC CAC CTG GTC
phe ser gly asp gly ser leu asp thr ala	thr ala ala arg leu ala asn his leu val
961/321	991/331
GAT CAG GGG TGC GAC GGT CTG GTG GTC TCG	GGC ACC ACC GGC GAG TCG CCG ACC ACC ACC
asp gln gly cys asp gly leu val val ser	gly thr thr gly glu ser pro thr thr thr

SEQ ID No.37F

FIGURE 37F

1021/341	GAC GGG GAG AAA ATC GAG CTG CTG CGG GCC	1051/351	GTC TTG GAA GCG GTG GGG GAC CGG GCC CGT
asp gly glu lys ile glu leu leu arg ala		val leu glu ala val gly asp arg ala arg	
1081/361	GTT ATC GCC GGT GCC GGC ACC TAT GAC ACC	1111/371	GCG CAC AGC ATC CGG CTG GCC AAG GCT TGT
val ile ala gly ala gly thr tyr asp thr		ala his ser ile arg leu ala lys ala cys	
1141/381	GCG GCC GAG GGT GCG CAC GGG CTG CTG GTG	1171/391	GTC ACG CCC TAC TAT TCC AAG CCG CCG CAG
ala ala glu gly ala his gly leu leu val		val thr pro tyr tyr ser lys pro pro gln	
1201/401	CGG GGG CTG CAA GCC CAT TTC ACC GCC GTC	1231/411	GCC GAC GCG ACC GAG CTG CCG ATG CTG CTC
arg gly leu gln ala his phe thr ala val		ala asp ala thr glu leu pro met leu leu	
1261/421	TAT GAC ATC CCG GGG CGG TCG GCG GTG CCG	1291/431	ATC GAG CCC GAC ACG ATC CGC GCG TTG GCG
tyr asp ile pro gly arg ser ala val pro		ile glu pro asp thr ile arg ala leu ala	
1321/441	TCG CAT CCG AAC ATC GTC GGA GTC AAG GAC	1351/451	GCC AAA GCC GAC CTG CAC AGC GGC GCC CAA
ser his pro asn ile val gly val lys asp		ala lys ala asp leu his ser gly ala gln	
1381/461	ATC ATG GCC GAC ACC GGA CTG GCC TAC TAT	1411/471	TCC GGC GAC GAC GCG CTC AAC CTG CCC TGG
ile met ala asp thr gly leu ala tyr tyr		ser gly asp asp ala leu asn leu pro trp	
1441/481	CTG GCC ATG GGC GCC ACG GGC TTC ATC AGC	1471/491	GTG ATT GCC CAC CTG GCA GCC GGG CAG CTT
leu ala met gly ala thr gly phe ile ser		val ile ala his leu ala ala gly gln leu	
1501/501	CGA GAG TTG TTG TCC GCC TTC GGT TCT GGG	1531/511	GAT ATC GCC ACC GCC CGC AAG ATC AAC ATT
arg glu leu leu ser ala phe gly ser gly		asp ile ala thr ala arg lys ile asn ile	
1561/521	GCG GTC GCC CCG CTG TGC AAC GCG ATG AGC	1591/531	CGC CTG GGT GGG GTG ACG TTG TCC AAG GCG
ala val ala pro leu cys asn ala met ser		arg leu gly gly val thr leu ser lys ala	
1621/541	GGC TTG CGG CTG CAG GGC ATC GAC GTC GGT	1651/551	GAT CCC CGG CTG CCC CAG GTG GCC GCG ACA
gly leu arg leu gln gly ile asp val gly		asp pro arg leu pro gln val ala ala thr	
1681/561	CCG GAG CAG ATC GAC GCG TTG GCC GCC GAC	1711/571	ATG CGC GCG GCC TCG GTG CTT CGG TGA
pro glu gln ile asp ala leu ala ala asp		met arg ala ala ser val leu arg OPA	

SEQ ID No.37F (continued 1)

FIGURE 37F (continued 1)

120/185

1/1	31/11
GCG GTG AAC TGG TGG GCC CGG ATG GTT CAA	GTA CGC CGT CGC AAA CTC GAG CAC AAC AGG
ala val asn trp trp ala arg met val gln	val arg arg arg lys leu glu his asn arg
61/21	91/31
AGA CGA CGG ATG GAA GGA GAT GCT GGC GCC	GGC CAG CTG AAC CCT GCC GAT GCG AAT AAG
arg arg arg met glu gly asp ala gly ala	gly gln leu asn pro ala asp ala asn lys
121/41	151/51
TCG TCG TCT ACG GAG GTG AAG GCG GCG GAT	TCG GCG GAA TCT GAC GCC GGA GCC GAC CAG
ser ser ser thr glu val lys ala ala asp	ser ala glu ser asp ala gly ala asp gln
181/61	211/71
ACT GGC CCG CAG GTG AAG GCG GCG GAT TCG	GCG GAA TCT GAC GCC GGA GAG CTC GGC GAG
thr gly pro gln val lys ala ala asp ser	ala glu ser asp ala gly glu leu gly glu
241/81	271/91
GAC GCG TGC CCA GAA CAG GCC CTC GTC GAG	CGG CGC CCG TCG CGG TTG CGG CGA GGC TGG
asp ala cys pro glu gln ala leu val glu	arg arg pro ser arg leu arg arg gly trp
301/101	331/111
CTT GTT GGC ATT GCG GCG ACG CTG CTC GCG	TTG GCC GGT GGC CTT GGC GCA GCG GGT TAT
leu val gly ile ala ala thr leu leu ala	leu ala gly gly leu gly ala ala gly tyr
361/121	391/131
TTT GCG TTG CGC TCA CAC CAG GAA AGC CAA	TCA ATC GCG CGC GAG GAC CTT GCG GCC ATT
phe ala leu arg ser his gln glu ser gln	ser ile ala arg glu asp leu ala ala ile
421/141	451/151
GAG GCC GCT AAG GAT TGC GTT GCG GCC ACG	CAG GCA CCC GAT GCT GGG GCG ATG TCG GCT
glu ala ala lys asp cys val ala ala thr	gln ala pro asp ala gly ala met ser ala
481/161	
AGC ATG CAG AAG ATC	
ser met gln lys ile	

SEQ ID No.38A

FIGURE 38A

1/1	31/11
CAG CGG TGA ACT GGT GGG CCC GGA TGG TTC	AAG TAC GCC GTC GCA AAC TCG AGC ACA ACA
gln arg OPA thr gly gly pro gly trp phe	lys tyr ala val ala asn ser ser thr thr
61/21	91/31
GGA GAC GAC GGA TGG AAG GAG ATG CTG GCG	CCG GCC AGC TGA ACC CTG CCG ATG CGA ATA
gly asp asp gly trp lys glu met leu ala	pro ala ser OPA thr leu pro met arg ile
121/41	151/51
AGT CGT CGT CTA CGG AGG TGA AGG CGG CGG	ATT CGG CGG AAT CTG ACG CCG GAG CCG ACC
ser arg arg leu arg arg OPA arg arg arg	ile arg arg arg asn leu thr pro glu pro thr
181/61	211/71
AGA CTG GCC CGC AGG TGA AGG CGG CGG ATT	CGG CGG AAT CTG ACG CCG GAG AGC TCG GCG
arg leu ala arg arg OPA arg arg arg ile	arg arg asn leu thr pro glu ser ser ala
241/81	271/91
AGG ACG CGT GCC CAG AAC AGG CCC TCG TCG	AGC GGC GCC CGT CGC GGT TGC GGC GAG GCT
arg thr arg ala gln asn arg pro ser ser	ser gly ala arg arg gly cys gly glu ala
301/101	331/111
GGC TTG TTG GCA TTG CGG CGA CGC TGC TCG	CGT TGG CCG GTG GCC TTG GCG CAG CGG GTT
gly leu leu ala leu arg arg arg cys ser	arg trp pro val ala leu ala gln arg val
361/121	391/131
ATT TTG CGT TGC GCT CAC ACC AGG AAA GCC	AAT CAA TCG CGC GCG AGG ACC TTG CGG CCA
ile leu arg cys ala his thr arg lys ala	asn gln ser arg ala arg thr leu arg pro
421/141	451/151
TTG AGG CCG CTA AGG ATT GCG TTG CGG CCA	CGC AGG CAC CCG ATG CTG GGG CGA TGT CGG
leu arg pro leu arg ile ala leu arg pro	arg arg his pro met leu gly arg cys arg
481/161	
CTA GCA TGC AGA AGA TC	
leu ala cys arg arg	

SEQ ID No.38B

FIGURE 38B

1/1
 AGC GGT GAA CTG GTG GGC CCG GAT GGT TCA AGT ACG CCG TCG CAA ACT CGA GCA CAA CAG
 ser gly glu leu val gly pro asp gly ser ser thr pro ser gln thr arg ala gln gln
 61/21
 GAG ACG ACG GAT GGA AGG AGA TGC TGG CGC CGG CCA GCT GAA CCC TGC CGA TGC GAA TAA
 glu thr thr asp gly arg arg cys trp arg arg pro ala glu pro cys arg cys glu OCH
 121/41
 GTC GTC GTC TAC GGA GGT GAA GGC GGC GGA TTC GGC GGA ATC TGA CGC CGG AGC CGA CCA
 val val val tyr gly gly glu gly gly gly phe gly gly ile OPA arg arg ser arg pro
 181/61
 GAC TGG CCC GCA GGT GAA GGC GGC GGA TTC GGC GGA ATC TGA CGC CGG AGA GCT CGG CGA
 asp trp pro ala gly glu gly gly gly phe gly gly ile OPA arg arg arg ala arg arg
 241/81
 GGA CGC GTG CCC AGA ACA GGC CCT CGT CGA GCG GCG CCC GTC GCG GTT GCG GCG AGG CTG
 gly arg val pro arg thr gly pro arg arg ala ala pro val ala val ala ala arg leu
 301/101
 GCT TGT TGG CAT TGC GGC GAC GCT GCT CGC GTT GGC CGG TGG CCT TGG CGC AGC GGG TTA
 ala cys trp his cys gly asp ala ala arg val gly arg trp pro trp arg ser gly leu
 361/121
 TTT TGC GTT GCG CTC ACA CCA GGA AAG CCA ATC AAT CGC GCG CGA GGA CCT TGC GGC CAT
 phe cys val ala leu thr pro gly lys pro ile asn arg ala arg gly pro cys gly his
 421/141
 TGA GGC CGC TAA GGA TTG CGT TGC GGC CAC GCA GGC ACC CGA TGC TGG GGC GAT GTC GGC
 OPA gly arg OCH gly leu arg cys gly his ala gly thr arg cys trp gly asp val gly
 481/161
 TAG CAT GCA GAA GAT C
 AMB his ala glu asp

SEQ ID No.38C

FIGURE 38C

Sequence Rv0175 predicted by Cole et al., 1998 (Nature 393 537-544) and containing seq38A

1/1	31/11
GTG AAG GCG GCG GAT TCG GCG GAA TCT GAC	GCC GGA GCC GAC CAG ACT GGC CCG CAG GTG
val lys ala ala asp ser ala glu ser asp	ala gly ala asp gln thr gly pro gln val
61/21	91/31
AAG GCG GCG GAT TCG GCG GAA TCT GAC	GCC GGA GAG CTC GGC GAG GAC GCG TGC CCA GAA
lys ala ala asp ser ala glu ser asp ala	gly glu leu gly glu asp ala cys pro glu
121/41	151/51
CAG GCC CTC GTC GAG CGG CGC CCG TCG CGG	TTG CGG CGA GGC TGG CTT GTT GGC ATT GCG
gln ala leu val glu arg arg pro ser arg	leu arg arg gly trp leu val gly ile ala
181/61	211/71
GCG ACG CTG CTC GCG TTG GCC GGT GGC CTT	GGC GCA GCG GGT TAT TTT GCG TTG CGC TCA
ala thr leu leu ala leu ala gly gly leu	gly ala ala gly tyr phe ala leu arg ser
241/81	271/91
CAC CAG GAA AGC CAA TCA ATC GCG CGC GAG	GAC CTT GCG GCC ATT GAG GCC GCT AAG GAT
his gln glu ser gln ser ile ala arg glu	asp leu ala ala ile glu ala ala lys asp
301/101	331/111
TGC GTT GCG GCC ACG CAG GCA CCC GAT GCT	GGG GCG ATG TCG GCT AGC ATG CAG AAG ATC
cys val ala ala thr gln ala pro asp ala	gly ala met ser ala ser met gln lys ile
361/121	391/131
ATC GAG TGT GGC ACC GGT GAT TTC GGT GCC	CAG GCG TCG TTG TAC ACC AGC ATG CTC GTC
ile glu cys gly thr gly asp phe gly ala	gln ala ser leu tyr thr ser met leu val
421/141	451/151
GAG GCG TAT CAA GCG GCC AGC GTC CAC GTG	CAA GTG ACC GAT ATG CGC GCG GCG GTC GAG
glu ala tyr gln ala ala ser val his val	gln val thr asp met arg ala ala val glu
481/161	511/171
CGC AAC AAC AAT GAC GGG TCG GTC GAT GTT	CTG GTG GCG CTC CGG GTC AAG GTG TCC AAC
arg asn asn asn asp gly ser val asp val	leu val ala leu arg val lys val ser asn
541/181	571/191
ACC GAC TCG GAT GCC CAT GAA GTC GGC TAC	CGT CTT CGG GTC CGG ATG GCA CTG GAT GAG
thr asp ser asp ala his glu val gly tyr	arg leu arg val arg met ala leu asp glu
601/201	631/211
GGC CGC TAT AAG ATC GCC AAA CTC GAC CAG	GTG ACG AAG TGA
gly arg tyr lys ile ala lys leu asp gln	val thr lys OPA

SEQ ID No.38D

FIGURE 38D

ORF according to Cole et al., 1998 (Nature 393 537-544) containing Rv0175

1/1	31/11
TGA ACT GGT GGG GCC GGA TGG TGT CAA GTA	CGC CGT CGC AAA CTC GAG CAC AAC AGG AGA
OPA thr gly gly ala gly trp cys gln val	arg arg arg lys leu glu his asn arg arg
61/21	91/31
CGA CGG ATG GAA GGA GAT GCT GGC GCC GGC	CAG CTG AAC CCT GCC GAT GCG AAT AAG TCG
arg arg met glu gly asp ala gly ala gly	gln leu asn pro ala asp ala asn lys ser
121/41	151/51
TCG TCT ACG GAG GTG AAG GCG GCG GAT TCG	GCG GAA TCT GAC GCC GGA GCC GAC CAG ACT
ser ser thr glu val lys ala ala asp ser	ala glu ser asp ala gly ala asp gln thr
181/61	211/71
GGC CCG CAG GTG AAG GCG GCG GAT TCG GCG	GAA TCT GAC GCC GGA GAG CTC GGC GAG GAC
gly pro gln val lys ala ala asp ser ala	glu ser asp ala gly glu leu gly glu asp
241/81	271/91
GCG TGC CCA GAA CAG GCC CTC GTC GAG CGG	CGC CCG TCG CGG TTG CGG CGA GGC TGG CTT
ala cys pro glu gln ala leu val glu arg	arg pro ser arg leu arg arg gly trp leu
301/101	331/111
GTT GGC ATT GCG GCG ACG CTG CTC GCG TTG	GCC GGT GGC CTT GGC GCA GCG GGT TAT TTT
val gly ile ala ala thr leu leu ala leu	ala gly gly leu gly ala ala gly tyr phe
361/121	391/131
GCG TTG CGC TCA CAC CAG GAA AGC CAA TCA	ATC GCG CGC GAG GAC CTT GCG GCC ATT GAG
ala leu arg ser his gln glu ser gln ser	ile ala arg glu asp leu ala ala ile glu
421/141	451/151
GCC GCT AAG GAT TGC GTT GCG GCC ACG CAG	GCA CCC GAT GCT GGG GCG ATG TCG GCT AGC
ala ala lys asp cys val ala ala thr gln	ala pro asp ala gly ala met ser ala ser
481/161	511/171
ATG CAG AAG ATC ATC GAG TGT GGC ACC GGT	GAT TTC GGT GCC CAG GCG TCG TTG TAC ACC
met gln lys ile ile glu cys gly thr gly	asp phe gly ala gln ala ser leu tyr thr
541/181	571/191
AGC ATG CTC GTC GAG GCG TAT CAA GCG GCC	AGC GTC CAC GTG CAA GTG ACC GAT ATG CGC
ser met leu val glu ala tyr gln ala ala	ser val his val gln val thr asp met arg
601/201	631/211
GCG GCG GTC GAG CGC AAC AAC AAT GAC GGG	TCG GTC GAT GTT CTG GTG GCG CTC CGG GTC
ala ala val glu arg asn asn asn asp gly	ser val asp val leu val ala leu arg val
661/221	691/231
AAG GTG TCC AAC ACC GAC TCG GAT GCC CAT	GAA GTC GGC TAC CGT CTT CGG GTC CGG ATG
lys val ser asn thr asp ser asp ala his	glu val gly tyr arg leu arg val arg met
721/241	751/251
GCA CTG GAT GAG GGC CGC TAT AAG ATC GCC	AAA CTC GAC CAG GTG ACG AAG TGA
ala leu asp glu gly arg tyr lys ile ala	lys leu asp gln val thr lys OPA

SEQ ID No.38F

FIGURE 38F

124/185

1/1 31/11
ACA CCT CCC CCC CCG CCG CCG CTG CCG CCG GTT CCC TTT CCC AAG GAA TGT CCG GCG CCG
thr pro pro pro pro pro pro leu pro pro val pro phe pro lys glu cys pro ala pro
61/21 91/31
GGC GTG ATG CAA GGC TGC CTT GAG AGC ACC AGC GGC TTG ATC ATG GGC ATC GAC AGC AAG
gly val met gln gly cys leu glu ser thr ser gly leu ile met gly ile asp ser lys
121/41 151/51
ACC GCA CTG GTC GCC GAG CGC ATC ACC GGT GCC GTC GAG GAG ATC
thr ala leu val ala glu arg ile thr gly ala val glu glu ile

SEQ ID No.39A

FIGURE 39A

1/1 31/11
CAC CTC CCC CCC CGC CGC CGC TGC CGC CGG TTC CCT TTC CCA AGG AAT GTC CGG CGC CGG
his leu pro pro arg arg arg cys arg arg phe pro phe pro arg asn val arg arg arg
61/21 91/31
GCG TGA TGC AAG GCT GCC TTG AGA GCA CCA GCG GCT TGA TCA TGG GCA TCG ACA GCA AGA
ala OPA cys lys ala ala leu arg ala pro ala ala OPA ser trp ala ser thr ala arg
121/41 151/51
CCG CAC TGG TCG CCG AGC GCA TCA CCG GTG CCG TCG AGG AGA TC
pro his trp ser pro ser ala ser pro val pro ser arg arg

SEQ ID No.39B

FIGURE 39B

1/1 31/11
GAC ACC TCC CCC CCC GCC GCC GCT GCC GCC GGT TCC CTT TCC CAA GGA ATG TCC GGC GCC
asp thr ser pro pro ala ala ala ala gly ser leu ser gln gly met ser gly ala
61/21 91/31
GGG CGT GAT GCA AGG CTG CCT TGA GAG CAC CAG CGG CTT GAT CAT GGG CAT CGA CAG CAA
gly arg asp ala arg leu pro OPA glu his gln arg leu asp his gly his arg gln gln
121/41 151/51
GAC CGC ACT GGT CGC CGA GCG CAT CAC CGG TGC CGT CGA GGA GAT C
asp arg thr gly arg arg ala his his arg cys arg arg gly asp

SEQ ID No.39C

FIGURE 39C

Coding sequence Rv3006 predicted by Cole et al., 1998 (Nature 393 537-544) and containing seq39A

1/1	31/11
ATG TGG ACA ACG CGG TTG GTT CGA TCC GGA	CTC GCC GCG CTG TGC GCG GCA GTG CTG GTA
Met trp thr thr arg leu val arg ser gly	leu ala ala leu cys ala ala val leu val
61/21	91/31
TCG AGC GGC TGC GCA CGG TTC AAC GAC GCT	CAA TCT CAG CCG TTC ACC ACC GAA CCG GAG
ser ser gly cys ala arg phe asn asp ala	gln ser gln pro phe thr thr glu pro glu
121/41	151/51
CTG CGG CCC CAA CCC AGC TCG ACA CCT CCC	CCC CCG CCG CCG CTG CCG CCG GTT CCC TTT
leu arg pro gln pro ser ser thr pro pro	pro pro pro pro leu pro pro val pro phe
181/61	211/71
CCC AAG GAA TGT CCG GCG CCG GGC GTG ATG	CAA GGC TGC CTT GAG AGC ACC AGC GGC TTG
pro lys glu cys pro ala pro gly val met	gln gly cys leu glu ser thr ser gly leu
241/81	271/91
ATC ATG GGC ATC GAC AGC AAG ACC GCA CTG	GTC GCC GAG CGC ATC ACC GGT GCC GTC GAG
ile met gly ile asp ser lys thr ala leu	val ala glu arg ile thr gly ala val glu
301/101	331/111
GAG ATC TCT ATC AGC GCC GAG CCG AAG GTA	AAG ACG GTC ATC CCC GTG GAT CCT GCC GGT
glu ile ser ile ser ala glu pro lys val	lys thr val ile pro val asp pro ala gly
361/121	391/131
GAC GGT GGC TTG ATG GAC ATT GTG CTG TCG	CCC ACC TAC TCG CAA GAC CGG CTG ATG TAC
asp gly gly leu met asp ile val leu ser	pro thr tyr ser gln asp arg leu met tyr
421/141	451/151
GCC TAC ATC AGC ACG CCC ACC GAC AAC CGG	GTG GTG CGA GTG GCC GAC GGC GAC ATC CCC
ala tyr ile ser thr pro thr asp asn arg	val val arg val ala asp gly asp ile pro
481/161	511/171
AAG GAC ATC CTG ACC GGC ATC CCC AAA GGT	GCT GCC GGT AAC ACC GGG GCG CTG ATC TTC
lys asp ile leu thr gly ile pro lys gly	ala ala gly asn thr gly ala leu ile phe
541/181	571/191
ACC AGT CCC ACC ACG CTG GTC GTG ATG ACC	GGG GAT GCT GGC GAC CCG GCG TTG GCC GCC
thr ser pro thr thr leu val val met thr	gly asp ala gly asp pro ala leu ala ala
601/201	631/211
GAT CCC CAA TCG TTG GCC GGT AAG GTC CTG	CGT ATC GAA CAG CCC ACC ACC ATC GGC CAG
asp pro gln ser leu ala gly lys val leu	arg ile glu gln pro thr thr ile gly gln
661/221	691/231
ACG CCG CCG ACG ACG GCG CTG TCT GGC ATC	GGC TCC GGC GGC GGC TTG TGC ATC GAT CCG
thr pro pro thr thr ala leu ser gly ile	gly ser gly gly gly leu cys ile asp pro
721/241	751/251
GTC GAC GGC TCG CTA TAT GTC GCC GAC CGC	ACG CCA ACG GCG GAC CGA TTG CAG CGC ATC
val asp gly ser leu tyr val ala asp arg	thr pro thr ala asp arg leu gln arg ile
781/261	811/271
ACC AAG AAC TCG GAG GTC TCT ACG GTA TGG	ACC TGG CCG GAC AAG CCC GGC GTG GCC GGG
thr lys asn ser glu val ser thr val trp	thr trp pro asp lys pro gly val ala gly
841/281	871/291
TGT GCC GCG ATG GAC GGC ACC GTG CTG GTC	AAC CTG ATT AAT ACC AAA CTG ACG GTG GCG
cys ala ala met asp gly thr val leu val	asn leu ile asn thr lys leu thr val ala
901/301	931/311
GTC CCG CTC GCG CCG TCG ACC GGT GCG GTC	ACC GGA GAA CCC GAC GTT GTC CGC AAA GAC
val arg leu ala pro ser thr gly ala val	thr gly glu pro asp val val arg lys asp
961/321	991/331
ACT CAT GCG CAT GCG TGG GCA TTA CGG ATG	TCG CCG GAC GGC AAC GTC TGG GGA GCC ACC
thr his ala his ala trp ala leu arg met	ser pro asp gly asn val trp gly ala thr
1021/341	1051/351
GTC AAC AAG ACC GCC GGC GAC GCC GAG AAG	CTC GAC GAT GTG GTG TTC CCG CTG TTC CCG
val asn lys thr ala gly asp ala glu lys	leu asp asp val val phe pro leu phe pro
1081/361	1111/371
CAG GGT GGC GGC TTC CCG CGC AAC AAC GAC	GAC AAG ACC TGA
gln gly gly gly phe pro arg asn asn asp	asp lys thr OPA

SEQ ID No.39D

FIGURE 39D

ORF according to Cole et al., 1998 (Nature 393 537-544) and containing Rv3006

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1/1                               31/11
TAA GGC CAT TTA GTG CCG AAT TGG GGA TTT GAG CGG CGC TTT CGC CAG ACA ATC CGC ACA
OCH gly his leu val pro asn trp gly phe glu arg arg phe arg gln thr ile arg thr
61/21                               91/31
TTG ACC CTG ACC AGC CCA CCA AAA GGC CCC AAT TGG GCC GCC ATG CCG ACA GTG CGC ACC
leu thr leu thr ser pro pro lys gly pro asn trp ala ala met pro thr val arg thr
121/41                               151/51
CCG GCA GGT GGC GGC GAT GCC CAC AAT GTC CGT AGC CTG TCG GTC ATG TGG ACA ACG CGG
pro ala gly gly gly asp ala his asn val arg ser leu ser val met trp thr thr arg
181/61                               211/71
TTG GTT CGA TCC GGA CTC GCC GCG CTG TGC GCG GCA GTG CTG GTA TCG AGC GGC TGC GCA
leu val arg ser gly leu ala ala leu cys ala ala val leu val ser ser gly cys ala
241/81                               271/91
CGG TTC AAC GAC GCT CAA TCT CAG CCG TTC ACC ACC GAA CCG GAG CTG CGG CCC CAA CCC
arg phe asn asp ala gln ser gln pro phe thr thr glu pro glu leu arg pro gln pro
301/101                               331/111
AGC TCG ACA CCT CCC CCC CCG CCG CCG CTG CCG CCG GTT CCC TTT CCC AAG GAA TGT CCG
ser ser thr pro pro pro pro pro pro pro leu pro pro val pro phe pro lys glu cys pro
361/121                               391/131
GCG CCG GGC GTG ATG CAA GGC TGC CTT GAG AGC ACC AGC GGC TTG ATC ATG GGC ATC GAC
ala pro gly val met gln gly cys leu glu ser thr ser gly leu ile met gly ile asp
421/141                               451/151
AGC AAG ACC GCA CTG GTC GCC GAG CGC ATC ACC GGT GCC GTC GAG GAG ATC TCT ATC AGC
ser lys thr ala leu val ala glu arg ile thr gly ala val glu glu ile ser ile ser
481/161                               511/171
GCC GAG CCG AAG GTA AAG ACG GTC ATC CCC GTG GAT CCT GCC GGT GAC GGT GGC TTG ATG
ala glu pro lys val lys thr val ile pro val asp pro ala gly asp gly gly leu met
541/181                               571/191
GAC ATT GTG CTG TCG CCC ACC TAC TCG CAA GAC CGG CTG ATG TAC GCC TAC ATC AGC ACG
asp ile val leu ser pro thr tyr ser gln asp arg leu met tyr ala tyr ile ser thr
601/201                               631/211
CCC ACC GAC AAC CGG GTG GTG CGA GTG GCC GAC GGC GAC ATC CCC AAG GAC ATC CTG ACC
pro thr asp asn arg val val arg val ala asp gly asp ile pro lys asp ile leu thr
661/221                               691/231
GGC ATC CCC AAA GGT GCT GCC GGT AAC ACC GGG GCG CTG ATC TTC ACC AGT CCC ACC ACG
gly ile pro lys gly ala ala gly asn thr gly ala leu ile phe thr ser pro thr thr
721/241                               751/251
CTG GTC GTG ATG ACC GGG GAT GCT GGC GAC CCG GCG TTG GCC GCC GAT CCC CAA TCG TTG
leu val val met thr gly asp ala gly asp pro ala leu ala ala asp pro gln ser leu
781/261                               811/271
GCC GGT AAG GTC CTG CGT ATC GAA CAG CCC ACC ACC ATC GGC CAG ACG CCG CCG ACG ACG
ala gly lys val leu arg ile glu gln pro thr thr ile gly gln thr pro pro thr thr
841/281                               871/291
GCG CTG TCT GGC ATC GGC TCC GGC GGC GGC TTG TGC ATC GAT CCG GTC GAC GGC TCG CTA
ala leu ser gly ile gly ser gly gly gly leu cys ile asp pro val asp gly ser leu
901/301                               931/311
TAT GTC GCC GAC CGC ACG CCA ACG GCG GAC CGA TTG CAG CGC ATC ACC AAG AAC TCG GAG
tyr val ala asp arg thr pro thr ala asp arg leu gln arg ile thr lys asn ser glu

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SEQ ID No.39F

FIGURE 39F

961/321 991/331
 GTC TCT ACG GTA TGG ACC TGG CCG GAC AAG CCC GGC GTG GCC GGG TGT GCC GCG ATG GAC
 val ser thr val trp thr trp pro asp lys pro gly val ala gly cys ala ala met asp
 1021/341 1051/351
 GGC ACC GTG CTG GTC AAC CTG ATT AAT ACC AAA CTG ACG GTG GCG GTC CGG CTC GCG CCG
 gly thr val leu val asn leu ile asn thr lys leu thr val ala val arg leu ala pro
 1081/361 1111/371
 TCG ACC GGT GCG GTC ACC GGA GAA CCC GAC GTT GTC CGC AAA GAC ACT CAT GCG CAT GCG
 ser thr gly ala val thr gly glu pro asp val val arg lys asp thr his ala his ala
 1141/381 1171/391
 TGG GCA TTA CGG ATG TCG CCG GAC GGC AAC GTC TGG GGA GCC ACC GTC AAC AAG ACC GCC
 trp ala leu arg met ser pro asp gly asn val trp gly ala thr val asn lys thr ala
 1201/401 1231/411
 GGC GAC GCC GAG AAG CTC GAC GAT GTG GTG TTC CCG CTG TTC CCG CAG GGT GGC GGC TTC
 gly asp ala glu lys leu asp asp val val phe pro leu phe pro gln gly gly gly phe
 1261/421
 CCG CGC AAC AAC GAC GAC AAG ACC TGA
 pro arg asn asn asp asp lys thr OPA

SEQ ID No.39F (continued)

FIGURE 39F (continued)

1/1 31/11
 GAA GGC CTT GTT GAG CCG GCG CAC GAA AAC GAT CGT TGT GTG TAC ATT GGT GTG TAT GGC
 glu gly leu val glu pro ala his glu asn asp arg cys val tyr ile gly val tyr gly
 61/21 91/31
 TCG GTT GAA CGT GTA TGT GCC CGA CGA ATT GGC GGA GCG CGC CAG GGC GCG GGG CTT GAA
 ser val glu arg val cys ala arg arg ile gly gly ala arg gln gly ala gly leu glu
 121/41 151/51
 CGT CTC GGC GCT GAC TCA GGC CGC GAT CAG TGC CGA GTT GGA GAA CTC CGC AAC CGA TGC
 arg leu gly ala asp ser gly arg asp gln cys arg val gly glu leu arg asn arg cys
 181/61 211/71
 GTG GCT TGA GGG GTT GGA ACC CAG AAG CAC CGG CGC TCG GCA TGA TGA CGT GCT GGG TGC
 val ala OPA gly val gly thr gln lys his arg arg ser ala OPA OPA arg ala gly cys
 241/81 271/91
 GAT CGA TGC CGC TCG CGA TGA GTT CGA AGC GTG AGA GCA TCG CCC ACT TCG CCG CCG GAG
 asp arg cys arg ser arg OPA val arg ser val arg ala ser pro thr ser pro pro glu
 301/101 331/111
 CAG GTG GTC GTC GAC GCG AGT GCC ATG GTG GAT C
 gln val val val asp ala ser ala met val asp

SEQ ID No.40A

FIGURE 40A

128/185

1/1	31/11
AAG GCC TTG TTG AGC CGG CGC ACG AAA ACG	ATC GTT GTG TGT ACA TTG GTG TGT ATG GCT
lys ala leu leu ser arg arg thr lys thr	ile val val cys thr leu val cys met ala
61/21	91/31
CGG TTG AAC GTG TAT GTG CCC GAC GAA TTG	GCG GAG CGC GCC AGG GCG CGG GGC TTG AAC
arg leu asn val tyr val pro asp glu leu	ala glu arg ala arg ala arg gly leu asn
121/41	151/51
GTC TCG GCG CTG ACT CAG GCC GCG ATC AGT	GCC GAG TTG GAG AAC TCC GCA ACC GAT GCG
val ser ala leu thr gln ala ala ile ser	ala glu leu glu asn ser ala thr asp ala
181/61	211/71
TGG CTT GAG GGG TTG GAA CCC AGA AGC ACC	GGC GCT CGG CAT GAT GAC GTG CTG GGT GCG
trp leu glu gly leu glu pro arg ser thr	gly ala arg his asp asp val leu gly ala
241/81	271/91
ATC GAT GCC GCT CGC GAT GAG TTC GAA GCG	TGA GAG CAT CGC CCA CTT CGC CGC CGG AGC
ile asp ala ala arg asp glu phe glu ala	OPA glu his arg pro leu arg arg arg ser
301/101	331/111
AGG TGG TCG TCG ACG CGA GTG CCA TGG TGG ATC	
arg trp ser ser thr arg val pro trp trp ile	

SEQ ID No.40B

FIGURE 40B

1/1	31/11
AGG CCT TGT TGA GCC GGC GCA CGA AAA CGA	TCG TTG TGT GTA CAT TGG TGT GTA TGG CTC
arg pro cys OPA ala gly ala arg lys arg	ser leu cys val his trp cys val trp leu
61/21	91/31
GGT TGA ACG TGT ATG TGC CCG ACG AAT TGG	CGG AGC GCG CCA GGG CGC GGG GCT TGA ACG
gly OPA thr cys met cys pro thr asn trp	arg ser ala pro gly arg gly ala OPA thr
121/41	151/51
TCT CGG CGC TGA CTC AGG CCG CGA TCA GTG	CCG AGT TGG AGA ACT CCG CAA CCG ATG CGT
ser arg arg OPA leu arg pro arg ser val	pro ser trp arg thr pro gln pro met arg
181/61	211/71
GGC TTG AGG GGT TGG AAC CCA GAA GCA CCG	GCG CTC GGC ATG ATG ACG TGC TGG GTG CGA
gly leu arg gly trp asn pro glu ala pro	ala leu gly met met thr cys trp val arg
241/81	271/91
TCG ATG CCG CTC GCG ATG AGT TCG AAG CGT	GAG AGC ATC GCC CAC TTC GCC GCC GGA GCA
ser met pro leu ala met ser ser lys arg	glu ser ile ala his phe ala ala gly ala
301/101	
GGT GGT CGT CGA CGC GAG TGC CAT GGT GGA TC	
gly gly arg arg arg glu cys his gly gly	

SEQ ID No.40C

FIGURE 40C

129/185

Coding sequence Rv0549c predicted by Cole et al., 1998 (Nature 393:537-544) and containing seq40A

1/1	31/11
gtg aga gca tcg ccc act tcg ccg ccg gag	cag gtg gtc gtc gac gcg agt gcc atg gtg
val arg ala ser pro thr ser pro pro glu	gln val val val asp ala ser ala met val
61/21	91/31
gat cta ctg gct cgc act agc gat ccg tgc	tct gcg gtg cgc gcg ccg ctg gct ccg acc
asp leu leu ala arg thr ser asp arg cys	ser ala val arg ala arg leu ala arg thr
121/41	151/51
gcg atg cac gcg ccg gcg cac ttc gat gca	gag gtg ttg tcg gcg ctg ggg cgc atg cag
ala met his ala pro ala his phe asp ala	glu val leu ser ala leu gly arg met gln
181/61	211/71
cgc gcc ggc gca ctc acc gtt gcc tat gtc	gat gcg gca ctg gag gag ttg cga cag gtg
arg ala gly ala leu thr val ala tyr val	asp ala ala leu glu glu leu arg gln val
241/81	271/91
ccg gtg act cga cac ggt ctt tcg tcg ctg	ctt gct gga gcg tgg tcg cgc cgc gac acc
pro val thr arg his gly leu ser ser leu	leu ala gly ala trp ser arg arg asp thr
301/101	331/111
ctc cgc ctg acc gat gcc ctc tac gtc gag	ctg gcc gaa acg gca ggt ctg gtg ttg ttg
leu arg leu thr asp ala leu tyr val glu	leu ala glu thr ala gly leu val leu leu
361/121	391/131
acc acc gac gaa aga ttg gca cgc gcc tgg	ccc tcg gct cac gcc atc ggc tga
thr thr asp glu arg leu ala arg ala trp	pro ser ala his ala ile gly OPA

SEQ ID No.40D

FIGURE 40D

ORF according to Cole et al., 1998 (Nature 393:537-544) and containing Rv0549c

1/1	31/11
tga gtt cga agc gtg aga gca tcg ccc act	tcg ccg ccg gag cag gtg gtc gtc gac gcg
OPA val arg ser val arg ala ser pro thr	ser pro pro glu gln val val val asp ala
61/21	91/31
agt gcc atg gtg gat cta ctg gct cgc act	agc gat ccg tgc tct gcg gtg cgc gcg ccg
ser ala met val asp leu leu ala arg thr	ser asp arg cys ser ala val arg ala arg
121/41	151/51
ctg gct ccg acc gcg atg cac gcg ccg gcg	cac ttc gat gca gag gtg ttg tcg gcg ctg
leu ala arg thr ala met his ala pro ala	his phe asp ala glu val leu ser ala leu
181/61	211/71
ggg cgc atg cag cgc gcc ggc gca ctc acc	gtt gcc tat gtc gat gcg gca ctg gag gag
gly arg met gln arg ala gly ala leu thr	val ala tyr val asp ala ala leu glu glu
241/81	271/91
ttg cga cag gtg ccg gtg act cga cac ggt	ctt tcg tcg ctg ctt gct gga gcg tgg tcg
leu arg gln val pro val thr arg his gly	leu ser ser leu leu ala gly ala trp ser
301/101	331/111
cgc cgc gac acc ctc cgc ctg acc gat gcc	ctc tac gtc gag ctg gcc gaa acg gca ggt
arg arg asp thr leu arg leu thr asp ala	leu tyr val glu leu ala glu thr ala gly
361/121	391/131
ctg gtg ttg ttg acc acc gac gaa aga ttg	gca cgc gcc tgg ccc tcg gct cac gcc atc
leu val leu leu thr thr asp glu arg leu	ala arg ala trp pro ser ala his ala ile
421/141	
ggc tga	
gly OPA	

SEQ ID No.40F

FIGURE 40F

REPLACEMENT SHEET (RULE 26)

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1/1                               31/11
CCT GGC CGG GAC GCC TAC GTG TAG CCC GCG GCT AGC ACA GGA TAG CCA TTG TTG TGC GGT
pro gly arg asp ala tyr val AMB pro ala ala ser thr gly AMB pro leu leu cys gly
61/21                               91/31
AGC GCC AAA ACG ATC AGC CCT TCG CGG ACA TGT CAG CAC CCG CCT TGG CCG GGA GAG CGG
ser ala lys thr ile ser pro ser arg thr cys gln his pro pro trp pro gly glu arg
121/41                               151/51
CGT CGT GAC CGT GCT GTC ACC ACG TCT GGT TAG GCT CGG GGC GCG GGC TGG CGC GGA GGA
arg arg asp arg ala val thr thr ser gly AMB ala arg gly ala gly trp arg gly gly
181/61                               211/71
GGT GTG TTG CGG AGG AGG TGT GTT GTA GTG GGG ACG GCG GAT CGG CCG TTG GAC GCC TCG
gly val leu arg arg arg cys val val val gly thr ala asp arg pro leu asp ala ser
241/81                               271/91
GCC TTG CGG GAC TGG GCA CAC GCC GTC GTC AGC GAT C
ala leu arg asp trp ala his ala val val ser asp

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SEQ ID No.41A

FIGURE 41A

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1/1                               31/11
CTG GCC GGG ACG CCT ACG TGT AGC CCG CGG CTA GCA CAG GAT AGC CAT TGT TGT GCG GTA
leu ala gly thr pro thr cys ser pro arg leu ala gln asp ser his cys cys ala val
61/21                               91/31
GCG CCA AAA CGA TCA GCC CTT CGC GGA CAT GTC AGC ACC CGC CTT GGC CGG GAG AGC GGC
ala pro lys arg ser ala leu arg gly his val ser thr arg leu gly arg glu ser gly
121/41                               151/51
GTC GTG ACC GTG CTG TCA CCA CGT CTG GTT AGG CTC GGG GCG CGG GCT GGC GCG GAG GAG
val val thr val leu ser pro arg leu val arg leu gly ala arg ala gly ala glu glu
181/61                               211/71
GTG TGT TGC GGA GGA GGT GTG TTG TAG TGG GGA CGG CGG ATC GGC CGT TGG ACG CCT CGG
val cys cys gly gly gly val leu AMB trp gly arg arg ile gly arg trp thr pro arg
241/81                               271/91
CCT TGC GGG ACT GGG CAC ACG CCG TCG TCA GCG ATC
pro cys gly thr gly his thr pro ser ser ala ile

```

SEQ ID No.41B

FIGURE 41B

```

1/1                               31/11
TGG CCG GGA CGC CTA CGT GTA GCC CGC GGC TAG CAC AGG ATA GCC ATT GTT GTG CGG TAG
trp pro gly arg leu arg val ala arg gly AMB his arg ile ala ile val val arg AMB
61/21                               91/31
CGC CAA AAC GAT CAG CCC TTC GCG GAC ATG TCA GCA CCC GCC TTG GCC GGG AGA GCG GCG
arg gln asn asp gln pro phe ala asp met ser ala pro ala leu ala gly arg ala ala
121/41                               151/51
TCG TGA CCG TGC TGT CAC CAC GTC TGG TTA GGC TCG GGG CGC GGG CTG GCG CGG AGG AGG
ser OPA pro cys cys his his val trp leu gly ser gly arg gly leu ala arg arg arg
181/61                               211/71
TGT GTT GCG GAG GAG GTG TGT TGT AGT GGG GAC GGC GGA TCG GCC GTT GGA CGC CTC GGC
cys val ala glu glu val cys cys ser gly asp gly gly ser ala val gly arg leu gly
241/81                               271/91
CTT GCG GGA CTG GGC ACA CGC CGT CGT CAG CGA TC
leu ala gly leu gly thr arg arg arg gln arg

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SEQ ID No.41C

FIGURE 41C

Coding sequence Rv2975c predicted by Cole et al, 1998 (Nature 393: 537-544) and containing seq41A

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1/1                               31/11
gtg ggg acg gcg gat cgg ccg ttg gac gcc tcg gcc ttg cgg gac tgg gca cac gcc gtc
val gly thr ala asp arg pro leu asp ala ser ala leu arg asp trp ala his ala val
61/21                               91/31
gtc agc gat ctg atc ctc cac atc gac gag atc aac cgg ctc aat gtg ttc ccg gtc gct
val ser asp leu ile leu his ile asp glu ile asn arg leu asn val phe pro val ala
121/41                               151/51
gac tcc gat acc ggc gtc aac atg ctg ttc acc atg cgt gcc gcg gtc gta gaa gct gat
asp ser asp thr gly val asn met leu phe thr met arg ala ala val val glu ala asp
181/61                               211/71
ttg cac gcg aat tcg cag gct gac gcc gaa gac gtg gcg cgg gtt gcg gcc gct ctc gcg
leu his ala asn ser gln ala asp ala glu asp val ala arg val ala ala leu ala
241/81
gcc ggc gcg cgt tga
ala gly ala arg OPA

```

SEQ ID No.41D

FIGURE 41D

ORF according to Cole et al, 1998 (Nature 393: 537-544) and containing Rv2975c

```

1/1                               31/11
tag gct cgg ggc gcg ggc tgg cgc gga gga ggt gtg ttg cgg agg agg tgt gtt gta gtg
AMB ala arg gly ala gly trp arg gly gly gly val leu arg arg arg cys val val val
61/21                               91/31
ggg acg gcg gat cgg ccg ttg gac gcc tcg gcc ttg cgg gac tgg gca cac gcc gtc gtc
gly thr ala asp arg pro leu asp ala ser ala leu arg asp trp ala his ala val val
121/41                               151/51
agc gat ctg atc ctc cac atc gac gag atc aac cgg ctc aat gtg ttc ccg gtc gct gac
ser asp leu ile leu his ile asp glu ile asn arg leu asn val phe pro val ala asp
181/61                               211/71
tcc gat acc ggc gtc aac atg ctg ttc acc atg cgt gcc gcg gtc gta gaa gct gat ttg
ser asp thr gly val asn met leu phe thr met arg ala ala val val glu ala asp leu
241/81                               271/91
cac gcg aat tcg cag gct gac gcc gaa gac gtg gcg cgg gtt gcg gcc gct ctc gcg gcc
his ala asn ser gln ala asp ala glu asp val ala arg val ala ala ala leu ala ala
301/101
ggc gcg cgt tga
gly ala arg OPA

```

SEQ ID No.41F

FIGURE 41F

sequence Rv 2974C predicted by Cole et al. (Nature 393:537-544) and which may be in the same reading frame as Seq41D. The sequencing of this region reveals, in one case out of three, a deletion of two nucleotides putting in phase observed in

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1/1                               31/11
ttg aac gga gct cgc ggc aac tcc ggc gtg atc ctg tcc cag atc ctg cgc ggg atc gca
leu asn gly ala arg gly asn ser gly val ile leu ser gln ile leu arg gly ile ala
61/21                               91/31
gag gtg acc gcg act gcg gcc gcc gcc tct ggc gcg gta ttg cgg gcg gtc gac gcc aac
glu val thr ala thr ala ala ala ala ser gly ala val leu arg ala val asp ala asn
121/41                               151/51
gcc ctc ggg gcc gcg ttg tgg cgc ggc gtc gag ttg gtc gtc gcg tcg atg ggt ggc gtg
ala leu gly ala ala leu trp arg gly val glu leu val val ala ser met gly gly val
181/61                               211/71
gag gtg ccg gga act atc gtc tcg gtg ctg cgg gcc gcc gcc gga gcc gtc gac cag tgc
glu val pro gly thr ile val ser val leu arg ala ala ala gly ala val asp gln cys
241/81                               271/91
gcg cac gag ggg ttg gcc ggt gcg gtc acc gcc gcc ggt gac gcg gcg gtc atc gcg ctg
ala his glu gly leu ala gly ala val thr ala ala gly asp ala ala val ile ala leu
301/101                               331/111
gaa aag acc ccc gaa cag ctt gac gtg ctc gcc gat gcg ggc gcg gtg gac gcc ggc gga
glu lys thr pro glu gln leu asp val leu ala asp ala gly ala val asp ala gly gly

```

SEQ ID No.41S

FIGURE 41S

361/121
 cgg ggc ctg ctg gtt ctg ctg gac gcg ttg cgc tcc acc atc tgc ggg cag gca cct gcc
 arg gly leu leu val leu leu asp ala leu arg ser thr ile cys gly gln ala pro ala
 421/141
 cgg gcg gtc tac gaa ccc tcg ccg cgc gcg ttg ccg acc gac acg gct acc caa cgc ccc
 arg ala val tyr glu pro ser pro arg ala leu pro thr asp thr ala thr gln arg pro
 481/161
 gcc ccg caa ttc gag gtg atg tat ctg ttg gcg gta tgt gat gct gca gcg gcg gac cag
 ala pro gln phe glu val met tyr leu leu ala val cys asp ala ala ala ala asp gln
 541/181
 ttg ccg gat cga ctc aag gaa ttg ggt gag tcg gtg gcc atc gcc gct gct ccg ccc gac
 leu arg asp arg leu lys glu leu gly glu ser val ala ile ala ala ala pro pro asp
 601/201
 agc tac tcc gta cac gtc cac acc gac gac gcc ggt gcc gcc gtg gaa gcc gga ttg gcg
 ser tyr ser val his val his thr asp asp ala gly ala ala val glu ala gly leu ala
 661/221
 gtg ggg cga gtt agc ccg atc gtg atc tcg gcg ctc ggt tcc ggg acc agc gga ttg ccg
 val gly arg val ser arg ile val ile ser ala leu gly ser gly thr ser gly leu pro
 721/241
 gcc ggt ggc tgg acg ccg ggc cgc gcc gtg ctg gcg gtc gtc gac ggc gac ggt gcc gcc
 ala gly gly trp thr arg gly arg ala val leu ala val val asp gly asp gly ala ala
 781/261
 gag ctg ttc gcc ggg gag ggc gcc tgc gtg ctg cga ccg ggt cca gac gcc gtg aca ccg
 glu leu phe ala gly glu gly ala cys val leu arg pro gly pro asp ala val thr pro
 841/281
 gcc gcc gat atc agt gcc cac cag ctg gtg ccg gcc gtg gta gac acc ggc gcc gcg cac
 ala ala asp ile ser ala his gln leu val arg ala val val asp thr gly ala ala his
 901/301
 gtg atg gtg ctg ccc aat ggc tat gtg gcc gcc gaa gaa ctg gtg gcc ggg tgt acc gcg
 val met val leu pro asn gly tyr val ala ala glu glu leu val ala gly cys thr ala
 961/321
 gcg atc ggc tgg ggc gtc gac gtg gta ccc gtg ccg acc gga tcg atg gtg cag ggg ttg
 ala ile gly trp gly val asp val val pro val pro thr gly ser met val gln gly leu
 1021/341
 gcc gcg ctg gcc gtg cat gac gcg gcc cgc cag gcc gtc gac gac ggc tac agc atg gcc
 ala ala leu ala val his asp ala ala arg gln ala val asp asp gly tyr ser met ala
 1081/361
 cgt gcc gcc ggt gct tcc ccg cac gga tcg gtg cgc att gcc acc caa aag gcg ctg acc
 arg ala ala gly ala ser arg his gly ser val arg ile ala thr gln lys ala leu thr
 1141/381
 tgg gcc ggt acc tgc aag ccg ggc gac ggt ctg ggt atc gcg ggc gac gag gtg ctg atc
 trp ala gly thr cys lys pro gly asp gly leu gly ile ala gly asp glu val leu ile
 1201/401
 gtc gcc gac gat gtc gcc gcg gcg gcc atc ggt ctg gtc gac ctg ttg ttg gca tcg gga
 val ala asp asp val ala ala ala ala ile gly leu val asp leu leu leu ala ser gly
 1261/421
 ggc gat ctg gtg acg gtg cta att ggc gcc ggc gta acc gaa gac gtg gct gtc gtc ctg
 gly asp leu val thr val leu ile gly ala gly val thr glu asp val ala val val leu
 1321/441
 gaa ccg cat gtg cac gac cac cat cca ggc acc gag ctg gtc tcc tac cgc acc gga cac
 glu arg his val his asp his his pro gly thr glu leu val ser tyr arg thr gly his
 1381/461
 cgc ggc gac gcg ctg ctg atc ggg gtc gag tag
 arg gly asp ala leu leu ile gly val glu AMB

SEQ ID No.41S (continued)

FIGURE 41S (continued)

REPLACEMENT SHEET (RULE 26)

Seq41T comprising seq 41F and seq 41S

1/1 31/11
tta ggc tgc ggg cgc ggg ctg gcg cgg agg agg tgt gtt gcg gag gag gtg tgt tgt agt
leu gly ser gly arg gly leu ala arg arg arg cys val ala glu val cys cys ser
AMB ala arg gly ala gly trp arg gly gly gly val leu arg arg arg cys val val val
arg leu gly ala arg ala gly ala glu glu val cys cys gly gly gly val leu AMB trp
61/21 91/31
ggg gac ggc gga tgc gcc gtt gga cgc ctc ggc ctt gcg gga ctg ggc aca cgc cgt cgt
gly asp gly gly ser ala val gly arg leu gly leu ala gly leu gly thr arg arg OPA
gly thr ala asp arg pro leu asp ala ser ala leu arg asp trp ala his ala val val
gly arg arg ile gly arg trp thr pro arg pro cys gly thr gly his thr pro ser ser
121/41 151/51
cag cga tct gat cct cca cat cga cga gat caa ccg gct caa tgt gtt ccc ggt cgc tga
gln arg ser asp pro pro his arg arg asp gln pro ala gln cys val pro gly arg OPA
ser asp leu ile leu his ile asp glu ile asn arg leu asn val phe pro val ala asp
ala ile OPA ser ser thr ser thr arg ser thr gly ser met cys ser arg ser leu thr
181/61 211/71
ctc cga tac cgg cgt caa cat gct gtt cac cat gcg tgc cgc ggt cgt aga agc tga ttt
leu arg tyr arg arg gln his ala val his his ala cys arg gly arg ser OPA phe
ser asp thr gly val asn met leu phe thr met arg ala ala val val glu ala asp leu
pro ile pro ala ser thr cys cys ser pro cys val pro arg ser AMB lys leu ile cys
241/81 271/91
gca cgc gaa ttc gca ggc tga cgc cga aga cgt ggc gcg ggt tgc ggc cgc tct cgc ggc
ala arg glu phe ala gly OPA arg arg arg arg gly ala gly cys gly arg ser arg gly
his ala asn ser gln ala asp ala glu asp val ala arg val ala ala leu ala ala
thr arg ile arg arg leu thr pro lys thr trp arg gly leu arg pro leu ser arg pro
301/101 331/111
cgg cgc gcg ttg aac gga gct cgc ggc aac tcc ggc gtg atc ctg tcc cag atc ctg cgc
arg arg ala leu asn gly ala arg gly asn ser gly val ile leu ser gln ile leu arg
gly ala arg OPA thr glu leu ala ala thr pro ala OPA ser cys pro arg ser cys ala
ala arg val glu arg ser ser arg gln leu arg arg asp pro val pro asp pro ala arg
361/121 391/131
ggg atc gca gag gtg acc gcg act gcg gcc gcc gcc tct ggc gcg gta ttg cgg gcg gtc
gly ile ala glu val thr ala thr ala ala ala ala ser gly ala val leu arg ala val
gly ser gln arg OPA pro arg leu arg pro pro leu ala arg tyr cys gly arg ser
asp arg arg gly asp arg asp cys gly arg arg leu trp arg gly ile ala gly gly arg
421/141 451/151
gac gcc aac gcc ctc ggg gcc gcg ttg tgg cgc ggc gtc gag ttg gtc gtc gcg tgc atg
asp ala asn ala leu gly ala ala leu trp arg gly val glu leu val val ala ser met
thr pro thr pro ser gly pro arg cys gly ala ala ser ser trp ser ser arg arg trp
arg gln arg pro arg gly arg val val ala arg arg arg val gly arg arg val asp gly
481/161 511/171
ggg ggc gtg gag gtg ccg gga act atc gtc tgc gtg ctg cgg gcc gcc gcc gga gcc gtc
gly gly val glu val pro gly thr ile val ser val leu arg ala ala ala gly ala val
val ala trp arg cys arg glu leu ser ser arg cys cys gly pro pro glu pro ser
trp arg gly gly ala gly asn tyr arg leu gly ala ala gly arg arg arg ser arg arg
541/181 571/191
gac cag tgc gcg cac gag ggg ttg gcc ggt gcg gtc acc gcc gcc ggt gac gcg gcg gtc
asp gln cys ala his glu gly leu ala gly ala val thr ala ala gly asp ala ala val
thr ser ala arg thr arg gly trp pro val arg ser pro pro val thr arg arg ser
pro val arg ala arg gly val gly arg cys gly his arg arg arg OPA arg gly gly his
601/201 631/211
atc gcg ctg gaa aag acc ccc gaa cag ctt gac gtg ctc gcc gat gcg ggc gcg gtg gac
ile ala leu glu lys thr pro glu gln leu asp val leu ala asp ala gly ala val asp
ser arg trp lys arg pro pro asn ser leu thr cys ser pro met arg ala arg trp thr
arg ala gly lys asp pro arg thr ala OPA arg ala arg arg cys gly arg gly gly arg
661/221 691/231
gcc ggc gga cgg ggc ctg ctg gtt ctg ctg gac gcg ttg cgc tcc acc atc tgc ggg cag
ala gly gly arg gly leu leu val leu leu asp ala leu arg ser thr ile cys gly gln
pro ala asp gly ala cys trp phe cys trp thr arg cys ala pro pro ser ala gly arg
arg arg thr gly pro ala gly ser ala gly arg val ala leu his his leu arg ala gly

SEQ ID No.41T

FIGURE 41T

REPLACEMENT SHEET (RULE 26)

721/241
gca cct gcc cgg gcg gtc tac gaa ccc tcg ccg cgc gcg ttg ccg acc gac acg gct acc
ala pro ala arg ala val tyr glu pro ser pro arg ala leu pro thr asp thr ala thr
his leu pro gly arg ser thr asn pro arg arg ala arg cys arg pro thr arg leu pro
thr cys pro gly gly leu arg thr leu ala ala arg val ala asp arg his gly tyr pro
781/261
caa cgc ccc gcc ccg caa ttc gag gtg atg tat ctg ttg gcg gta tgt gat gct gca gcg
gln arg pro ala pro gln phe glu val met tyr leu leu ala val cys asp ala ala ala
asn ala pro pro arg asn ser arg OPA cys ile cys trp arg tyr val met leu gln arg
thr pro arg pro ala ile arg gly asp val ser val gly gly met OPA cys cys ser gly
841/281
gcg gac cag ttg ccg gat cga ctc aag gaa ttg ggt gag tcg gtg gcc atc gcc gct gct
ala asp gln leu arg asp arg leu lys glu leu gly glu ser val ala ile ala ala ala
arg thr ser cys gly ile asp ser arg asn trp val ser arg trp pro ser pro leu leu
gly pro val ala gly ser thr gln gly ile gly OPA val gly gly his arg arg cys ser
901/301
ccg ccc gac agc tac tcc gta cac gtc cac acc gac gac gcc ggt gcc gcc gtg gaa gcc
pro pro asp ser tyr ser val his val his thr asp asp ala gly ala ala val glu ala
arg pro thr ala thr pro tyr thr ser thr pro thr thr pro val pro trp lys pro
ala arg gln leu leu arg thr arg pro his arg arg arg arg cys arg arg gly ser arg
961/321
gga ttg gcg gtg ggg cga gtt agc cgg atc gtg atc tcg gcg ctc ggt tcc ggg acc agc
gly leu ala val gly arg val ser arg ile val ile ser ala leu gly ser gly thr ser
asp trp arg trp gly glu leu ala gly ser OPA ser arg arg ser val pro gly pro ala
ile gly gly ala ser AMB pro asp arg asp leu gly ala arg phe arg asp gln arg
1021/341
gga ttg ccg gcc ggt ggc tgg acg cgg gcc cgc gcc gtg ctg gcg gtc gtc gac ggc gac
gly leu pro ala gly gly trp thr arg gly arg ala val leu ala val val asp gly asp
asp cys arg pro val ala gly arg gly ala ala pro cys trp arg ser ser thr ala thr
ile ala gly arg trp leu asp ala gly pro arg arg ala gly gly arg arg arg arg
1081/361
ggt gcc gcc gag ctg ttc gcc ggg gag ggc gcc tgc gtg ctg cga ccg ggt cca gac gcc
gly ala ala glu leu phe ala gly glu gly ala cys val leu arg pro gly pro asp ala
val pro pro ser cys ser pro gly arg ala pro ala cys cys asp arg val gln thr pro
cys arg arg ala val arg arg gly gly arg leu arg ala ala thr gly ser arg arg arg
1141/381
gtg aca ccg gcc gcc gat atc agt gcc cac cag ctg gtg ccg gcc gtg gta gac acc ggc
val thr pro ala ala asp ile ser ala his gln leu val arg ala val val asp thr gly
OPA his arg pro pro ile ser val pro thr ser trp cys gly pro trp AMB thr pro ala
asp thr gly arg arg tyr gln cys pro pro ala gly ala gly arg gly arg his arg arg
1201/401
gcc gcg cac gtg atg gtg ctg ccc aat ggc tat gtg gcc gcc gaa gaa ctg gtg gcc ggg
ala ala his val met val leu pro asn gly tyr val ala ala glu glu leu val ala gly
pro arg thr OPA trp cys cys pro met ala met trp pro pro lys asn trp trp pro gly
arg ala arg asp gly ala ala gln trp leu cys gly arg arg arg thr gly gly arg val
1261/421
tgt acc gcg gcg atc ggc tgg ggc gtc gac gtg gta ccc gtg ccg acc gga tcg atg gtg
cys thr ala ala ile gly trp gly val asp val val pro val pro thr gly ser met val
val pro arg arg ser ala gly ala ser thr trp tyr pro cys arg pro asp arg trp cys
tyr arg gly asp arg leu gly arg arg arg arg ala asp arg ile asp gly ala
1321/441
cag ggg ttg gcc gcg ctg gcc gtg cat gac gcg gcc cgc cag gcc gtc gac gac ggc tac
gln gly leu ala ala leu ala val his asp ala ala arg gln ala val asp asp gly tyr
arg gly trp pro arg trp pro cys met thr arg pro ala arg pro ser thr thr ala thr
gly val gly arg ala gly arg ala OPA arg gly pro pro gly arg arg arg arg leu gln
1381/461
agc atg gcc cgt gcc gcc ggt gct tcc ccg cac gga tcg gtg cgc att gcc acc caa aag
ser met ala arg ala ala gly ala ser arg his gly ser val arg ile ala thr gln lys
ala trp pro val pro pro val leu pro gly thr asp arg cys ala leu pro pro lys arg
his gly pro cys arg arg cys phe pro ala arg ile gly ala his cys his pro lys gly

SEQ ID No.41T (continued 1)

FIGURE 41T (continued 1)

1441/481
gcg ctg acc tgg gcc ggt acc tgc aag ccg ggc gac ggt ctg ggt atc gcg ggc gac gag
ala leu thr trp ala gly thr cys lys pro gly asp gly leu gly ile ala gly asp glu
arg OPA pro gly pro val pro ala ser arg ala thr val trp val ser arg ala thr arg
ala asp leu gly arg tyr leu gln ala gly arg arg ser gly tyr arg gly arg arg gly
1501/501
gtg ctg atc gtc gcc gac gat gtc gcc gcg gcg gcc atc ggt ctg gtc gac ctg ttg ttg
val leu ile val ala asp asp val ala ala ala ile gly leu val asp leu leu leu
cys OPA ser ser pro thr met ser pro arg arg pro ser val trp ser thr cys cys trp
ala asp arg arg arg arg cys arg arg gly gly his arg ser gly arg pro val val gly
1561/521
gca tcg gga ggc gat ctg gtg acg gtg cta att ggc gcc ggc gta acc gaa gac gtg gct
ala ser gly gly asp leu val thr val leu ile gly ala gly val thr glu asp val ala
his arg glu ala ile trp OPA arg cys OCH leu ala pro ala OCH pro lys thr trp leu
ile gly arg arg ser gly asp gly ala asn trp arg arg arg asn arg arg arg gly cys
1621/541
gtc gtc ctg gaa ccg cat gtg cac gac cac cat cca gcc acc gag ctg gtc tcc tac ccg
val val leu glu arg his val his asp his his pro gly thr glu leu val ser tyr arg
ser ser trp asn gly met cys thr thr thr ile gln ala pro ser trp ser pro thr ala
arg pro gly thr ala cys ala arg pro pro ser arg his arg ala gly leu leu pro his
1681/561
acc gga cac ccg ggc gac gcg ctg ctg atc ggg gtc gag tag
thr gly his arg gly asp ala leu leu ile gly val glu AMB
pro asp thr ala ala thr arg cys OPA ser gly ser ser
arg thr pro arg arg arg ala ala asp arg gly arg val

SEQ ID No.41T (continued 2)

FIGURE 41T (continued 2)

1/1	31/11
GCC GGT AAC GCC GCG TCC CAG TGC TAT CCG	TCC GCC GGA CCG CCC GAA ACA TCA GCG GCG
ala gly asn ala ala ser gln cys tyr pro	ser ala gly pro pro glu thr ser ala ala
61/21	91/31
GGC GCC CCG GTC GGC CGC GGC CGG GCT CGA	CCC GCT CCA CCT GGC CAT CAG CGA CCA GGT
gly ala pro val gly arg gly arg ala arg	pro ala pro pro gly his gln arg pro gly
121/41	151/51
TAT CGA GGT GGA AGC GGA CGG TGT TGG GAT	GCA CGC CCA ACT TGC CGG CGA TCG CGG CGA
tyr arg gly gly ser gly arg cys trp asp	ala arg pro thr cys arg arg ser arg arg
181/61	211/71
TGC TCA TCG GAA CCC GCG ACG CAC ACA ATG	CCC GCA GCA CCG CAC GAC GGC GCC CCA CCG
cys ser ser glu pro ala thr his thr met	pro ala ala pro his asp gly ala pro pro
241/81	271/91
GCT CTT GCA GTG ACC TGA TGA TGA CAC TCA	CCC CCA TAA GGC TCG TCG GCT GCG CCT GAG
ala leu ala val thr OPA OPA OPA his ser	pro pro OCH gly ser ser ala ala pro glu
301/101	331/111
CAA TGC AGT AAG TTT ACA CAA ACG GAC TTG	TAA AAA CCT GCG GAG GTG GGG TCT ATG GCC
gln cys ser lys phe thr gln thr asp leu	OCH lys pro ala glu val gly ser met ala
361/121	391/131
AAC AAA CGT GGC AAT GCC GGG CAG CCT CTG	CCC TTG TCG GAT C
asn lys arg gly asn ala gly gln pro leu	pro leu ser asp

SEQ ID No.42A

FIGURE 42A

137/185

1
1/1 31/11
CCG GTA ACG CCG CGT CCC AGT GCT ATC CGT CCG CCG GAC CGC CCG AAA CAT CAG CGG CGG
pro val thr pro arg pro ser ala ile arg pro pro asp arg pro lys his gln arg arg
61/21 91/31
GCG CCC CCG TCG GCC GCG GCC GGG CTC GAC CCG CTC CAC CTG GCC ATC AGC GAC CAG GTT
ala pro arg ser ala ala ala gly leu asp pro leu his leu ala ile ser asp gln val
121/41 151/51
ATC GAG GTG GAA GCG GAC GGT GTT GGG ATG CAC GCC CAA CTT GCC GGC GAT CGC GGC GAT
ile glu val glu ala asp gly val gly met his ala gln leu ala gly asp arg gly asp
181/61 211/71
GCT CAT CGG AAC CCG CGA CGC ACA CAA TGC CCG CAG CAC CGC ACG ACG GCG CCC CAC CGG
ala his arg asn pro arg arg thr gln cys pro gln his arg thr thr ala pro his arg
241/81 271/91
CTC TTG CAG TGA CCT GAT GAT GAC ACT CAC CCC CAT AAG GCT CGT CGG CTG CGC CTG AGC
leu leu gln OPA pro asp asp asp thr his pro his lys ala arg arg leu arg leu ser
301/101 331/111
AAT GCA GTA AGT TTA CAC AAA CGG ACT TGT AAA AAC CTG CGG AGG TGG GGT CTA TGG CCA
asn ala val ser leu his lys arg thr cys lys asn leu arg arg trp gly leu trp pro
361/121 391/131
ACA AAC GTG GCA ATG CCG GGC AGC CTC TGC CCT TGT CGG ATC
thr asn val ala met pro gly ser leu cys pro cys arg ile

SEQ ID No.42B

FIGURE 42B

1/1 31/11
CGG TAA CGC CGC GTC CCA GTG CTA TCC GTC CGC CGG ACC GCC CGA AAC ATC AGC GGC GGG
arg OCH arg arg val pro val leu ser val arg arg thr ala arg asn ile ser gly gly
61/21 91/31
CGC CCC GGT CGG CCG CGG CCG GGC TCG ACC CGC TCC ACC TGG CCA TCA GCG ACC AGG TTA
arg pro gly arg pro arg pro gly ser thr arg ser thr trp pro ser ala thr arg leu
121/41 151/51
TCG AGG TGG AAG CGG ACG GTG TTG GGA TGC ACG CCC AAC TTG CCG GCG ATC GCG GCG ATG
ser arg trp lys arg thr val leu gly cys thr pro asn leu pro ala ile ala ala met
181/61 211/71
CTC ATC GGA ACC CGC GAC GCA CAC AAT GCC CGC AGC ACC GCA CGA CGG CGC CCC ACC GGC
leu ile gly thr arg asp ala his asn ala arg ser thr ala arg arg arg pro thr gly
241/81 271/91
TCT TGC AGT GAC CTG ATG ATG ACA CTC ACC CCC ATA AGG CTC GTC GGC TGC GCC TGA GCA
ser cys ser asp leu met met thr leu thr pro ile arg leu val gly cys ala OPA ala
301/101 331/111
ATG CAG TAA GTT TAC ACA AAC GGA CTT GTA AAA ACC TGC GGA GGT GGG GTC TAT GGC CAA
met gln OCH val tyr thr asn gly leu val lys thr cys gly gly gly val tyr gly gln
361/121 391/131
CAA ACG TGG CAA TGC CGG GCA GCC TCT GCC CTT GTC GGA TC
gln thr trp gln cys arg ala ala ser ala leu val gly

SEQ ID No.42C

FIGURE 42C

Coding sequence Rv2622 predicted by Cole et al., 1998 (Nature 393:537-544) and containing seq42A:

1/1	31/11
atg gcc aac aaa cgt ggc aat gcc ggg cag	cct ctg ccc ttg tcg gat cga gac gac gac
Met ala asn lys arg gly asn ala gly gln	pro leu pro leu ser asp arg asp asp asp
61/21	91/31
cac atg cag ggg cac tgg ctg ctg gcc cgg	ctg ggc aag cgg gtg ctg cgt ccc ggc ggc
his met gln gly his trp leu leu ala arg	leu gly lys arg val leu arg pro gly gly
121/41	151/51
gtc gaa ctc acc cgg aca ctg ctg gcc cgc	gcc gag gtg acc gac gcc gac gtg ctc gag
val glu leu thr arg thr leu leu ala arg	ala glu val thr asp ala asp val leu glu
181/61	211/71
ctg gca ccg ggc ctg ggc cgc acc gca gcc	gaa atc ttg gcc cgc aac ccg cgg tcg tac
leu ala pro gly leu gly arg thr ala ala	glu ile leu ala arg asn pro arg ser tyr
241/81	271/91
gtg ggg gcg gag agc gat ccc aac gcg gcc	aac ctg gtc cga cac gtt ctc gcc ggc cgc
val gly ala glu ser asp pro asn ala ala	asn leu val arg his val leu ala gly arg
301/101	331/111
ggc gac gtc cgg gtc acc gac gcg gcc gat	acc gga tta tcc gac gcc agc gcc gat gtc
gly asp val arg val thr asp ala ala asp	thr gly leu ser asp ala ser ala asp val
361/121	391/131
gtc atc ggc gag gcg atg ctg acc atg caa	ggc aac gcg gct aaa cac acg atc gtc gcc
val ile gly glu ala met leu thr met gln	gly asn ala ala lys his thr ile val ala
421/141	451/151
gag gcg gcg cgg gtg ctg agg ccg ggt ggc	cgc tac gcg att cac gaa cta gcg ctg gtg
glu ala ala arg val leu arg pro gly gly	arg tyr ala ile his glu leu ala leu val
481/161	511/171
ccg gac gac gtc gca gag cag gtc cgc acc	gac ctg cgg cag tcg ctg gcc cgc gcg ctc
pro asp asp val ala glu gln val arg thr	asp leu arg gln ser leu ala arg ala leu
541/181	571/191
aag gtc aat gcg cgt ccg ctg acc gtt gcg	gaa tgg tcg cac ctc tta gcg ggc cat gga
lys val asn ala arg pro leu thr val ala	glu trp ser his leu leu ala gly his gly
601/201	631/211
ctg gtc gtc gaa cac gtt gtc acc gct tcc	atg gcg ttg tta caa ccg cga cgg gtg atc
leu val val glu his val val thr ala ser	met ala leu leu gln pro arg arg val ile
661/221	691/231
gct gac gaa ggc ctc ctg ggt gcg ctg cgg	ttc gcc gga aac ctg ctc atc cat cgt gcc
ala asp glu gly leu leu gly ala leu arg	phe ala gly asn leu leu ile his arg ala
721/241	751/251
gcg cgt cgg cga gtc ctg ttg atg cgc cac	aca ttc cgc agg cat cgt gaa cgc ttg aca
ala arg arg arg val leu leu met arg his	thr phe arg arg his arg glu arg leu thr
781/261	811/271
gcc gtc gcc att gtc gcg cac aaa ccg cac	gtc gat tcg tga
ala val ala ile val ala his lys pro his	val asp ser OPA

SEQ ID No.42D

FIGURE 42D

ORF according to Cole et al., 1998 (Nature 393:537-544) and containing Rv2622

1/1	31/11
taa aaa cct gcg gag gtg ggg tct atg gcc	aac aaa cgt ggc aat gcc ggg cag cct ctg
OCH lys pro ala glu val gly ser met ala	asn lys arg gly asn ala gly gln pro leu
61/21	91/31
ccc ttg tcg gat cga gac gac gac cac atg	cag ggg cac tgg ctg ctg gcc cgg ctg ggc
pro leu ser asp arg asp asp asp his met	gln gly his trp leu leu ala arg leu gly
121/41	151/51
aag cgg gtg ctg cgt ccc ggc ggc gtc gaa	ctc acc cgg aca ctg ctg gcc cgc gcc gag
lys arg val leu arg pro gly gly val glu	leu thr arg thr leu leu ala arg ala glu
181/61	211/71
gtg acc gac gcc gac gtg ctc gag ctg gca	ccg ggc ctg ggc cgc acc gca gcc gaa atc
val thr asp ala asp val leu glu leu ala	pro gly leu gly arg thr ala ala glu ile
241/81	271/91
ttg gcc cgc aac ccg cgg tcg tac gtg ggg	gcg gag agc gat ccc aac gcg gcc aac ctg
leu ala arg asn pro arg ser tyr val gly	ala glu ser asp pro asn ala ala asn leu
301/101	331/111
gtc cga cac gtt ctc gcc ggc cgc ggc gac	gtc cgg gtc acc gac gcg gcc gat acc gga
val arg his val leu ala gly arg gly asp	val arg val thr asp ala ala asp thr gly
361/121	391/131
tta tcc gac gcc agc gcc gat gtc gtc atc	ggc gag gcg atg ctg acc atg caa ggc aac
leu ser asp ala ser ala asp val val ile	gly glu ala met leu thr met gln gly asn
421/141	451/151
gcg gct aaa cac acg atc gtc gcc gag gcg	gcg cgg gtg ctg agg ccg ggt ggc cgc tac
ala ala lys his thr ile val ala glu ala	ala arg val leu arg pro gly gly arg tyr
481/161	511/171
gcg att cac gaa cta gcg ctg gtg ccg gac	gac gtc gca gag cag gtc cgc acc gac ctg
ala ile his glu leu ala leu val pro asp	asp val ala glu gln val arg thr asp leu
541/181	571/191
cgg cag tcg ctg gcc cgc gcg ctc aag gtc	aat gcg cgt ccg ctg acc gtt gcg gaa tgg
arg gln ser leu ala arg ala leu lys val	asn ala arg pro leu thr val ala glu trp
601/201	631/211
tcg cac ctc tta gcg ggc cat gga ctg gtc	gtc gaa cac gtt gtc acc gct tcc atg gcg
ser his leu leu ala gly his gly leu val	val glu his val val thr ala ser met ala
661/221	691/231
ttg tta caa ccg cga cgg gtg atc gct gac	gaa ggc ctc ctg ggt gcg ctg cgg ttc gcc
leu leu gln pro arg arg val ile ala asp	glu gly leu leu gly ala leu arg phe ala
721/241	751/251
gga aac ctg ctc atc cat cgt gcc gcg cgt	cgg cga gtc ctg ttg atg cgc cac aca ttc
gly asn leu leu ile his arg ala ala arg	arg arg val leu leu met arg his thr phe
781/261	811/271
cgc agg cat cgt gaa cgc ttg aca gcc gtc	gcc att gtc gcg cac aaa ccg cac gtc gat
arg arg his arg glu arg leu thr ala val	ala ile val ala his lys pro his val asp
841/281	
tcg tga	
ser OPA	

SEQ ID No.42F

FIGURE 42F


```

1/1                               31/11
atc gcg cgt gac atc gat gac cag ggt cgg ctg tgt ctg gac gtc ggc ggt cga acg gta
ile ala arg asp ile asp asp gln gly arg leu cys leu asp val gly gly arg thr val
61/21                               91/31
gtt gtt tca gcg ggc gac gtg gtg cat ttg cgt taa ctc gcg cgg agc tgg cgt ccc caa
val val ser ala gly asp val val his leu arg OCH leu ala arg ser trp arg pro gln
121/41                               151/51
aag att aag gtc gcg ggc atg agc tat ccg gag aat gtc ctg gcc gct ggc gag cag gtc
lys ile lys val ala gly met ser tyr pro glu asn val leu ala ala gly glu gln val
181/61                               211/71
gtt ctg cac cgc cat ccg cac tgg aat cgc tta atc tgg ccc gtc gtg gtg ctg gtc ttg
val leu his arg his pro his trp asn arg leu ile trp pro val val val leu val leu
241/81                               271/91
ctg acc ggg ttg gcg gcg ttc ggg tcc gga ttc gtc aac tcg aca cct tgg cag cag atc
leu thr gly leu ala ala phe gly ser gly phe val asn ser thr pro trp gln gln ile

```

SEQ ID No.43A

FIGURE 43A

```

1/1                               31/11
tcg cgc gtg aca tcg atg acc agg gtc ggc tgt gtc tgg acg tcg gcg gtc gaa cgg tag
ser arg val thr ser met thr arg val gly cys val trp thr ser ala val glu arg AMB
61/21                               91/31
ttg ttt cag cgg gcg acg tgg tgc att tgc gtt aac tcg cgc gga gct ggc gtc ccc aaa
leu phe gln arg ala thr trp cys ile cys val asn ser arg gly ala gly val pro lys
121/41                               151/51
aga tta agg tcg cgg gca tga gct atc ccg aga atg tcc tgg ccg ctg gcg agc agg tcg
arg leu arg ser arg ala OPA ala ile arg arg met ser trp pro leu ala ser arg ser
181/61                               211/71
ttc tgc acc gcc atc cgc act gga atc gct taa tct ggc ccg tcg tgg tgc tgg tct tgc
phe cys thr ala ile arg thr gly ile ala OCH ser gly pro ser trp cys trp ser cys
241/81                               271/91
tga ccg ggt tgg cgg cgt tcg ggt ccg gat tcg tca act cga cac ctt ggc agc aga tc
OPA pro gly trp arg arg ser gly pro asp ser ser thr arg his leu gly ser arg

```

SEQ ID No.43B

FIGURE 43B

141/185

1/1	31/11
cgc gcg tga cat cga tga cca ggg tcg gct	gtg tct gga cgt cgg cgg tcg aac ggt agt
arg ala OPA his arg OPA pro gly ser ala	val ser gly arg arg arg ser asn gly ser
61/21	91/31
tgt ttc agc ggg cga cgt ggt gca ttt gcg	tta act cgc gcg gag ctg gcg tcc cca aaa
cys phe ser gly arg arg gly ala phe ala	leu thr arg ala glu leu ala ser pro lys
121/41	151/51
gat taa ggt cgc ggg cat gag cta tcc gga	gaa tgt cct ggc cgc tgg cga gca ggt cgt
asp OCH gly arg gly his glu leu ser gly	glu cys pro gly arg trp arg ala gly arg
181/61	211/71
tct gca ccg cca tcc gca ctg gaa tcg ctt	aat ctg gcc cgt cgt ggt gct ggt ctt gct
ser ala pro pro ser ala leu glu ser leu	asn leu ala arg arg gly ala gly leu ala
241/81	271/91
gac cgg gtt ggc ggc gtt cgg gtc cgg att	cgt caa ctc gac acc ttg gca gca gat c
asp arg val gly gly val arg val arg ile	arg gln leu asp thr leu ala ala asp

SEQ ID No.43C

FIGURE 43C

Coding sequence Rv3278c predicted by Cole et al., 1998 (Nature 393:537-544) and containing seq43A:

1/1	31/11
atg agc tat ccg gag aat gtc ctg gcc gct	ggc gag cag gtc gtt ctg cac cgc cat ccg
Met ser tyr pro glu asn val leu ala ala	gly glu gln val val leu his arg his pro
61/21	91/31
cac tgg aat cgc tta atc tgg ccc gtc gtg	gtg ctg gtc ttg ctg acc ggg ttg gcg gcg
his trp asn arg leu ile trp pro val val	val leu val leu leu thr gly leu ala ala
121/41	151/51
ttc ggg tcc gga ttc gtc aac tcg aca cct	tgg cag cag atc gct aag aac gtg att cac
phe gly ser gly phe val asn ser thr pro	trp gln gln ile ala lys asn val ile his
181/61	211/71
gcg gtc atc tgg ggg atc tgg ttg gtg atc	gtc gcc tgg ctc acg ctg tgg cca ttc ctg
ala val ile trp gly ile trp leu val ile	val gly trp leu thr leu trp pro phe leu
241/81	271/91
agc tgg ctg acc aca cat ttc gtg gtg acc	aac cgg cgg gtg atg ttc cgg cat ggt gtg
ser trp leu thr thr his phe val val thr	asn arg arg val met phe arg his gly val
301/101	331/111
ctg acc cgc agc ggg atc gac ata ccg cta	gca cgg atc aac agc gtg gag ttc cgg gac
leu thr arg ser gly ile asp ile pro leu	ala arg ile asn ser val glu phe arg asp
361/121	391/131
cgg atc ttc gag cgg att ttt cgc acc ggg	acg ttg att atc gag tcc gcg tca caa gat
arg ile phe glu arg ile phe arg thr gly	thr leu ile ile glu ser ala ser gln asp
421/141	451/151
ccg ctc gag ttc tac aac att ccg cgc ctg	cgg gag gtg cat gcg ttg ctg tat cac gag
pro leu glu phe tyr asn ile pro arg leu	arg glu val his ala leu leu tyr his glu
481/161	511/171
ggt ttc gac acc ctg ggc tcc gac gag tcg	ccc agc tga
val phe asp thr leu gly ser asp glu ser	pro ser OPA

SEQ ID No.43D

FIGURE 43D

ORF according to Cole et al., 1998 (Nature 393:537-544) and containing Rv3278c

1/1	31/11
taa ctc gcg cgg agc tgg cgt ccc caa aag	att aag gtc gcg ggc atg agc tat ccg gag
OCH leu ala arg ser trp arg pro gln lys	ile lys val ala gly met ser tyr pro glu
61/21	91/31
aat gtc ctg gcc gct ggc gag cag gtc gtt	ctg cac cgc cat ccg cac tgg aat cgc tta
asn val leu ala ala gly glu gln val val	leu his arg his pro his trp asn arg leu
121/41	151/51
atc tgg ccc gtc gtg gtg ctg gtc ttg ctg	acc ggg ttg gcg gcg ttc ggg tcc gga ttc
ile trp pro val val val leu val leu leu	thr gly leu ala ala phe gly ser gly phe
181/61	211/71
gtc aac tcg aca cct tgg cag cag atc gct	aag aac gtg att cac gcg gtc atc tgg ggg
val asn ser thr pro trp gln gln ile ala	lys asn val ile his ala val ile trp gly
241/81	271/91
atc tgg ttg gtg atc gtc ggc tgg ctc acg	ctg tgg cca ttc ctg agc tgg ctg acc aca
ile trp leu val ile val gly trp leu thr	leu trp pro phe leu ser trp leu thr thr
301/101	331/111
cat ttc gtg gtg acc aac cgg cgg gtg atg	ttc cgg cat ggt gtg ctg acc cgc agc ggg
his phe val val thr asn arg arg val met	phe arg his gly val leu thr arg ser gly
361/121	391/131
atc gac ata ccg cta gca cgg atc aac agc	gtg gag ttc cgg gac cgg atc ttc gag cgg
ile asp ile pro leu ala arg ile asn ser	val glu phe arg asp arg ile phe glu arg
421/141	451/151
att ttt cgc acc ggg acg ttg att atc gag	tcc gcg tca caa gat ccg ctc gag ttc tac
ile phe arg thr gly thr leu ile ile glu	ser ala ser gln asp pro leu glu phe tyr
481/161	511/171
aac att ccg cgc ctg cgg gag gtg cat gcg	ttg ctg tat cac gag gtt ttc gac acc ctg
asn ile pro arg leu arg glu val his ala	leu leu tyr his glu val phe asp thr leu
541/181	
ggc tcc gac gag tcg ccc agc tga	
gly ser asp glu ser pro ser OPA	

SEQ ID No.43F

FIGURE 43F

1/1	31/11
cca aga tgg atg tct acc aac gca ccg ccg ccg gct ggc agc cgc tca aga ccg gta tca	
pro arg trp met ser thr asn ala pro pro pro ala gly ser arg ser arg pro val ser	
61/21	91/31
cca ccc ata tcg gtt cgg cgg gca tgg cgc ccg aag cca aga gcg gat atc cgg cca ctc	
pro pro ile ser val arg arg ala trp arg arg lys pro arg ala asp ile arg pro leu	
121/41	151/51
cga tgg ggg ttt aca gcc tgg act ccg ctt ttg gca ccg cgc cga atc ccg gtg gcg ggt	
arg trp gly phe thr ala trp thr pro leu leu ala pro arg arg ile pro val ala gly	
181/61	211/71
tgc cgt ata ccc aag tcg gac cca atc act ggt gga gtg gcg acg aca ata gcc cca cct	
cys arg ile pro lys ser asp pro ile thr gly gly val ala thr thr ile ala pro pro	
241/81	271/91
tta act cca tgc agg tct gtc aga agt ccc agt gcc cgt tca gca ccg ccg aca gcg aga	
leu thr pro cys arg ser val arg ser pro ser ala arg ser ala arg pro thr ala arg	
301/101	331/111
acc tgc aaa tcc cgc agt aca agc att cgg tcg tga tgg gcg tca aca agg cca agg tcc	
thr cys lys ser arg ser thr ser ile arg ser opa trp ala ser thr arg pro arg ser	
361/121	391/131
cag gca aag gct ccg cgt tct tct ttc aca cca ccg acg gcg ggc cca ccg ccg gtt gtg	
gln ala lys ala pro arg ser ser phe thr pro pro thr ala gly pro pro arg val val	
421/141	
tgg cga tc	
trp arg	

FIGURE 44A

[illegible]

FIGURE 44B

SEQ ID No.44C

REPLACEMENT SHEET WITH E 26

Coding sequence Rv0309 predicted by Cole et al., 1998 (Nature 393:537-544) and containing Seq44A:

```

1/1                               31/11
atg agc cga ctc cta gct ttg ctg tgc gct gcg gta tgc acg ggc tgc gtt gct gtg gtt
Met ser arg leu leu ala leu leu cys ala ala val cys thr gly cys val ala val val
61/21                               91/31
ctc gcg cca gtg agc ctg gcc gtc gtc aac ccg tgg ttc gcg aac tcg gtc ggc aat gcc
leu ala pro val ser leu ala val val asn pro trp phe ala asn ser val gly asn ala
121/41                               151/51
act cag gtg gtt tcg gtg gtg gga acc ggc ggt tcg acg gcc aag atg gat gtc tac caa
thr gln val val ser val val gly thr gly gly ser thr ala lys met asp val tyr gln
181/61                               211/71
cgc acc gcc gcc ggc tgg cag ccg ctc aag acc ggt atc acc acc cat atc ggt tcg gcg
arg thr ala ala gly trp gln pro leu lys thr gly ile thr thr his ile gly ser ala
241/81                               271/91
ggc atg gcg ccg gaa gcc aag agc gga tat ccg gcc act ccg atg ggg gtt tac agc ctg
gly met ala pro glu ala lys ser gly tyr pro ala thr pro met gly val tyr ser leu
301/101                               331/111
gac tcc gct ttt ggc acc gcg ccg aat ccc ggt ggc ggg ttg ccg tat acc caa gtc gga
asp ser ala phe gly thr ala pro asn pro gly gly gly leu pro tyr thr gln val gly
361/121                               391/131
ccc aat cac tgg tgg agt ggc gac gac aat agc ccc acc ttt aac tcc atg cag gtc tgt
pro asn his trp trp ser gly asp asp asn ser pro thr phe asn ser met gln val cys
421/141                               451/151
cag aag tcc cag tgc ccg ttc agc acg gcc gac agc gag aac ctg caa atc ccg cag tac
gln lys ser gln cys pro phe ser thr ala asp ser glu asn leu gln ile pro gln tyr
481/161                               511/171
aag cat tcg gtc gtg atg ggc gtc aac aag gcc aag gtc cca ggc aaa ggc tcc gcg ttc
lys his ser val val met gly val asn lys ala lys val pro gly lys gly ser ala phe
541/181                               571/191
ttc ttt cac acc acc gac ggc ggg ccc acc gcg ggt tgt gtg gcg atc gac gat gcc acg
phe phe his thr thr asp gly gly pro thr ala gly cys val ala ile asp asp ala thr
601/201                               631/211
ctg gtg cag atc atc cgt tgg ctg cgg cct ggt gcg gtg atc gcg atc gcc aag taa
leu val gln ile ile arg trp leu arg pro gly ala val ile ala ile ala lys OCH

```

SEQ ID No.44D

FIGURE 44D

ORF according to Cole et al., 1998 (Nature 393:537-544) and containing Rv0309

1/1
tga gcg atg agc cga ctc cta gct ttg ctg tgc gct gcg gta tgc acg ggc tgc gtt gct
OPA ala met ser arg leu leu ala leu leu cys ala ala val cys thr gly cys val ala
61/21
gtg gtt ctc gcg cca gtg agc ctg gcc gtc gtc aac ccg tgg ttc gcg aac tcg gtc ggc
val val leu ala pro val ser leu ala val val asn pro trp phe ala asn ser val gly
121/41
aat gcc act cag gtg gtt tcg gtg gtg gga acc ggc ggt tcg acg gcc aag atg gat gtc
asn ala thr gln val val ser val val gly thr gly gly ser thr ala lys met asp val
181/61
tac caa cgc acc gcc gcc ggc tgg cag ccg ctc aag acc ggt atc acc acc cat atc ggt
tyr gln arg thr ala ala gly trp gln pro leu lys thr gly ile thr thr his ile gly
241/81
tcg gcg ggc atg gcg ccg gaa gcc aag agc gga tat ccg gcc act ccg atg ggg gtt tac
ser ala gly met ala pro glu ala lys ser gly tyr pro ala thr pro met gly val tyr
301/101
agc ctg gac tcc gct ttt ggc acc gcg ccg aat ccc ggt ggc ggg ttg ccg tat acc caa
ser leu asp ser ala phe gly thr ala pro asn pro gly gly gly leu pro tyr thr gln
361/121
gtc gga ccc aat cac tgg tgg agt ggc gac gac aat agc ccc acc ttt aac tcc atg cag
val gly pro asn his trp trp ser gly asp asp asn ser pro thr phe asn ser met gln
421/141
gtc tgt cag aag tcc cag tgc ccg ttc agc acg gcc gac agc gag aac ctg caa atc ccg
val cys gln lys ser gln cys pro phe ser thr ala asp ser glu asn leu gln ile pro
481/161
cag tac aag cat tcg gtc gtg atg ggc gtc aac aag gcc aag gtc cca ggc aaa ggc tcc
gln tyr lys his ser val val met gly val asn lys ala lys val pro gly lys gly ser
541/181
gcg ttc ttc ttt cac acc acc gac ggc ggg ccc acc gcg ggt tgt gtg gcg atc gac gat
ala phe phe phe his thr thr asp gly gly pro thr ala gly cys val ala ile asp asp
601/201
gcc acg ctg gtg cag atc atc cgt tgg ctg ccg cct ggt gcg gtg atc gcg atc gcc aag
ala thr leu val gln ile ile arg trp leu arg pro gly ala val ile ala ile ala lys
661/221
taa
OCH

SEQ ID No.44F

FIGURE 44F

Cloned fragment fused with phoA

1/1 31/11
 gat ctc ccc gga cac cag gtc atc cgg cga gat ggt gat cga ggc tcg gac ccg cag gca
 asp leu pro gly his gln val ile arg arg asp gly asp arg gly ser asp pro gln ala
 61/21 91/31
 tcc ggt agc cag agg cac cag cat cag caa cat cgc gat ggc cag cat gcc gcg ccg tcg
 ser gly ser gln arg his gln his gln gln his arg asp gly gln his ala ala pro ser
 121/41 151/51
 ggt cct tgc cac tcg cga tcc ttg gga tga cgg tgg ggc ata gct agc gcg cac cag gtc
 gly pro cys his ser arg ser leu gly OPA arg trp gly ile ala ser ala his gln val
 181/61 211/71
 atc gtg cca gac cgg gca tgc cgc gtc ggc aag ctg tcg ggc gcg ggt tag agc ggt agc
 ile val pro asp arg ala cys arg val gly lys leu ser gly ala gly AMB ser gly ser
 241/81 271/91
 gtg cga ccc agg atg gcg aat gct cgg ggg tca ccg gcg aag tgg tag ccg ccg atg atg
 val arg pro arg met ala asn ala arg gly ser pro ala lys trp AMB pro arg met met
 301/101 331/111
 tcg gtg aag ccc aac cgg cgg tac aac cgc cac gcc cga ttg tcc tca ccg ttg gtc tcc
 ser val lys pro asn arg arg tyr asn arg his ala arg leu ser ser pro leu val ser
 361/121 391/131
 ggt gtg gag agc agg acg ttg tcc tcg tcg cga ccg gct agc agt cgg ccg gcc aac gcc
 gly val glu ser arg thr leu ser ser ser arg pro ala ser ser arg arg ala asn ala
 421/141 451/151
 tcc ccg agg cca cgg cct tga gcg cgg gga agg atg tgc aat tca gtc aac tcg aag tag
 ser pro arg pro arg pro OPA ala arg gly arg met cys asn ser val asn ser lys AMB
 481/161 511/171
 ctg gtc atc agt cgg gcg atc gct agg cgc gga aag ccg ctg cgt tgc aag ccc agt acc
 leu val ile ser arg ala ile ala arg arg gly lys pro leu arg cys lys pro ser thr
 541/181 571/191
 acc tgc tgt tgc cac cac tgg ccg ggc gcc ccg gga tag ccg tac gcc act ccg agc att
 thr cys cys cys his his trp pro gly ala pro gly AMB pro tyr ala thr pro ser ile
 601/201 631/211
 ggc gcg ttg ctc agt tcg gcg gcc gac ggc agc gcc gtg gtg tcg gcg gcc tcg gcc tgt
 gly ala leu leu ser ser ala ala asp gly ser ala val val ser ala ala ser ala cys
 661/221 691/231
 tcg gct gcc gtt acc tcg acg gcc gcg acc gcc tgc cag ccg cgc cgc ccg atg tgc tcc
 ser ala ala val thr ser thr ala ala thr ala cys gln pro arg arg arg met cys ser
 721/241 751/251
 agc cac att ggg gcg cgc aaa gtc tcg gtg ccc ctg ggg tag cgc atc gcg tcg aca tac
 ser his ile gly ala arg lys val ser val pro leu gly AMB arg ile ala ser thr tyr
 781/261 811/271
 acc gtc agg gca tca ccg agg ccg cgc tcc ata tcg ctg ggc ggc aga tcg atg agg aat
 thr val arg ala ser pro arg arg arg ser ile ser leu gly gly arg ser met arg asn
 841/281 871/291
 atc gcc aac gcg cgg tgt cct cct cat gtg atg aac cga tgc gtg ctt gcg cac cag tat
 ile ala asn ala arg cys pro pro his val met asn arg cys val leu ala his gln tyr
 901/301 931/311
 cgg aca agc cga tga ggc cgc ccg cgc tgg acg ggg ctt gta gcg tat ggc cgt ttc cgc
 arg thr ser arg OPA gly arg pro arg trp thr gly leu val ala tyr gly arg phe arg

SEQ ID No.45ZA

FIGURE 45ZA

961/321
 tca gct cgt cgc tgc ggc gcc gcc ggg ata gaa tcg ccc gcg aac cag tgg tac ggc gca
 ser ala arg arg cys gly ala ala gly ile glu ser pro ala asn gln trp tyr gly ala
 1021/341
 gat tga cct cgt atc atc tga gtt agt tgc ccg cgc aat ggg cat ccg cgt gtt atc ggt
 asp OPA pro arg ile ile OPA val ser cys pro arg asn gly his pro arg val ile gly
 1081/361
 att acg tga cag tct gtc ggc aag gag gga cgc atg cca ctg tcc gat cat gag cag cgg
 ile thr OPA gln ser val gly lys glu gly arg met pro leu ser asp his glu gln arg
 1141/381
 atg ctt gac cag atc gag agc gct ctg tac gcc gaa gat ccc aag ttc gca tcg agt gtc
 met leu asp gln ile glu ser ala leu tyr ala glu asp pro lys phe ala ser ser val
 1201/401
 cgt ggc ggg ggc ttc cgc gca ccg acc gcg cgg cgg cgc ctg cag ggc gcg gcg ttg ttc
 arg gly gly gly phe arg ala pro thr ala arg arg arg leu gln gly ala ala leu phe
 1261/421
 atc atc ggt ctg ggg atg ttg gtt tcc ggc gtg gcg ttc aaa gag acc atg atc gga agt
 ile ile gly leu gly met leu val ser gly val ala phe lys glu thr met ile gly ser
 1321/441
 ttc ccg ata ctg agc gtt ttc ggt ttt gtc gtg atg ttc ggt ggt gtg gtg tat gcc atc
 phe pro ile leu ser val phe gly phe val val met phe gly gly val val tyr ala ile
 1381/461
 acc ggt cct cgg ttg tcc ggc agg atg gat cgt ggc gga tcg gct gct ggg gct tcg cgc
 thr gly pro arg leu ser gly arg met asp arg gly gly ser ala ala gly ala ser arg
 1441/481
 cag cgt cgt acc aag ggg gcc ggg ggc tca ttc acc agc cgt atg gaa gat c
 gln arg arg thr lys gly ala gly gly ser phe thr ser arg met glu asp

SEQ ID No.45ZA (continued)

FIGURE 45ZA (continued)

fragment seq452A shifted minus 1 for the reading frame

1/1	31/11
atc tcc ccg gac acc agg tca tcc ggc gag	atg gtg atc gag gct cgg acc cgc agg cat
ile ser pro asp thr arg ser ser gly glu	met val ile glu ala arg thr arg arg his
61/21	91/31
ccg gta gcc aga ggc acc agc atc agc aac	atc gcg atg gcc agc atg ccg cgc cgt cgg
pro val ala arg gly thr ser ile ser asn	ile ala met ala ser met pro arg arg arg
121/41	151/51
gtc ctt gcc act cgc gat cct tgg gat gac	ggg ggc gca tag cta gcg cgc acc agg tca
val leu ala thr arg asp pro trp asp asp	gly gly ala AMB leu ala arg thr arg ser
181/61	211/71
tcg tgc cag acc ggg cat gcc gcg tcg gca	agg tgt cgg gcg cgg gtt aga gcg gta gcg
ser cys gln thr gly his ala ala ser ala	ser cys arg ala arg val arg ala val ala
241/81	271/91
tgc gac cca gga tgg cga atg ctc ggg ggt	cac cgg cga agt ggt agc cgc gga tga tgt
cys asp pro gly trp arg met leu gly gly	his arg arg ser gly ser arg gly OPA cys
301/101	331/111
cgg tga agc cca acc ggc ggt aca acc gcc	acg ccc gat tgt cct cac cgt tgg tct ccg
arg OPA ser pro thr gly gly thr thr ala	thr pro asp cys pro his arg trp ser pro
361/121	391/131
gtg tgg aga gca gga cgt tgt cct cgt cgc	gac cgg cta gca gtc ggc ggg cca acg cct
val trp arg ala gly arg cys pro arg arg	asp arg leu ala val gly gly pro thr pro
421/141	451/151
ccc cga ggc cac ggc ctt gag cgc ggg gaa	gga tgt gca att cag tca act cga agt agc
pro arg gly his gly leu glu arg gly glu	gly cys ala ile gln ser thr arg ser ser
481/161	511/171
tgg tca tca gtc ggg cga tcg cta ggc gcg	gaa agc cgc tgc gtt gca agc cca gta cca
trp ser ser val gly arg ser leu gly ala	glu ser arg cys val ala ser pro val pro
541/181	571/191
cct gct gtt gcc acc act ggc cgg gcg ccc	cgg gat agc cgt acg cca ctc cga gca ttg
pro ala val ala thr thr gly arg ala pro	arg asp ser arg thr pro leu arg ala leu
601/201	631/211
gcg cgt tgc tca gtt cgg cgg ccg acg gca	gcg ccg tgg tgt cgg cgg cct cgg cct gtt
ala arg cys ser val arg arg pro thr ala	ala pro trp cys arg arg pro arg pro val
661/221	691/231
cgg ctg ccg tta cct cga cgg ccg cga ccg	cct gcc agc cgc gcc gcc gga tgt gct cca
arg leu pro leu pro arg arg pro arg pro	pro ala ser arg ala ala gly cys ala pro
721/241	751/251
gcc aca ttg ggg cgc gca aag tct cgg tgc	ccc tgg ggt agc gca tcg cgt cga cat aca
ala thr leu gly arg ala lys ser arg cys	pro trp gly ser ala ser arg arg his thr
781/261	811/271
ccg tca ggg cat cac cga ggc ggc gct cca	tat cgc tgg gcg gca gat cga tga gga ata
pro ser gly his his arg gly gly ala pro	tyr arg trp ala ala asp arg OPA gly ile
841/281	871/291
tcg cca acg cgc ggt gtc ctc ctc atg tga	tga acc gat gcg tgc ttg cgc acc agt atc
ser pro thr arg gly val leu leu met OPA	OPA thr asp ala cys leu arg thr ser ile
901/301	931/311
gga caa gcc gat gag gcc gcc cgc gct gga	cgg ggc ttg tag cgt atg gcc gtt tcc gct
gly gln ala asp glu ala ala arg ala gly	arg gly leu AMB arg met ala val ser ala
961/321	991/331
cag ctc gtc gct gcg gcg ccg ccg gga tag	aat cgc ccg cga acc agt ggt acg gcg cag
gln leu val ala ala ala pro pro gly AMB	asn arg pro arg thr ser gly thr ala gln

SEQ ID No.452B

FIGURE 452B

DEPT. 4 CEMENT SHEET ADHESION

151/185

fragment seq452A shifted minus 2 for the reading frame

1/1	31/11
tct ccc cgg aca cca ggt cat ccg gcg aga	tgg tga tcg agg ctc gga ccc gca ggc atc
ser pro arg thr pro gly his pro ala arg	trp OPA ser arg leu gly pro ala gly ile
61/21	91/31
cgg tag cca gag gca cca gca tca gca aca	tcg cga tgg cca gca tgc cgc gcc gtc ggg
arg AMB pro glu ala pro ala ser ala thr	ser arg trp pro ala cys arg ala val gly
121/41	151/51
tcc ttg cca ctc gcg atc ctt ggg atg acg	gtg ggg cat agc tag cgc gca cca ggt cat
ser leu pro leu ala ile leu gly met thr	val gly his ser AMB arg ala pro gly his
181/61	211/71
cgt gcc aga ccg ggc atg ccg cgt cgg caa	gct gtc ggg cgc ggg tta gag cgg tag cgt
arg ala arg pro gly met pro arg arg gln	ala val gly arg gly leu glu arg AMB arg
241/81	271/91
gcg acc cag gat ggc gaa tgc tcg ggg gtc	acc ggc gaa gtg gta gcc gcg gat gat gtc
ala thr gln asp gly glu cys ser gly val	thr gly glu val val ala ala asp asp val
301/101	331/111
ggt gaa gcc caa ccg gcg gta caa ccg cca	cgc ccg att gtc ctc acc gtt ggt ctc cgg
gly glu ala gln pro ala val gln pro pro	arg pro ile val leu thr val gly leu arg
361/121	391/131
tgt gga gag cag gac gtt gtc ctc gtc gcg	acc ggc tag cag tcg gcg ggc caa cgc ctc
cys gly glu gln asp val val leu val ala	thr gly AMB gln ser ala gly gln arg leu
421/141	451/151
ccc gag gcc acg gcc ttg agc gcg ggg aag	gat gtg caa ttc agt caa ctc gaa gta gct
pro glu ala thr ala leu ser ala gly lys	asp val gln phe ser gln leu glu val ala
481/161	511/171
ggt cat cag tcg ggc gat cgc tag gcg cgg	aaa gcc gct gcg ttg caa gcc cag tac cac
gly his gln ser gly asp arg AMB ala arg	lys ala ala ala leu gln ala gln tyr his
541/181	571/191
ctg ctg ttg cca cca ctg gcc ggg cgc ccc	ggg ata gcc gta cgc cac tcc gag cat tgg
leu leu leu pro pro leu ala gly arg pro	gly ile ala val arg his ser glu his trp
601/201	631/211
cgc gtt gct cag ttc ggc ggc cga cgg cag	cgc cgt ggt gtc ggc ggc ctc ggc ctg ttc
arg val ala gln phe gly gly arg arg gln	arg arg gly val gly gly leu gly leu phe
661/221	691/231
ggc tgc cgt tac ctc gac ggc cgc gac cgc	ctg cca gcc gcg ccg ccg gat gtg ctc cag
gly cys arg tyr leu asp gly arg asp arg	leu pro ala ala pro pro asp val leu gln
721/241	751/251
cca cat tgg ggc gcg caa agt ctc ggt gcc	cct ggg gta gcg cat cgc gtc gac ata cac
pro his trp gly ala gln ser leu gly ala	pro gly val ala his arg val asp ile his
781/261	811/271
cgt cag ggc atc acc gag gcg gcg ctc cat	atc gct ggg cgg cag atc gat gag gaa tat
arg gln gly ile thr glu ala ala leu his	ile ala gly arg gln ile asp glu glu tyr
841/281	871/291
cgc caa cgc gcg gtg tcc tcc tca tgt gat	gaa ccg atg cgt gct tgc gca cca gta tcg
arg gln arg ala val ser ser ser cys asp	glu pro met arg ala cys ala pro val ser
901/301	931/311
gac aag ccg atg agg ccg ccc gcg ctg gac	ggg gct tgt agt gta tgg ccg ttt ccg ctc
asp lys pro met arg pro pro ala leu asp	gly ala cys ser val trp pro phe pro leu

SEQ ID No.452C

FIGURE 452C

961/321
 agc tcg tcg ctg cgg cgc cgc cgg gat aga atc gcc cgc gaa cca gtg gta cgg cgc aga
 ser ser ser leu arg arg arg arg asp arg ile ala arg glu pro val val arg arg arg
 1021/341
 ttg acc tcg tat cat ctg agt tag ttg ccc gcg caa tgg gca tcc gcg tgt tat cgg tat
 leu thr ser tyr his leu ser AMB leu pro ala gln trp ala ser ala cys tyr arg tyr
 1081/361
 tac gtg aca gtc tgt cgg caa gga ggg acg cat gcc act ctc cga tca tga gca gcg gat
 tyr val thr val cys arg gln gly gly thr his ala thr leu arg ser OPA ala ala asp
 1141/381
 gct tga cca gat cga gag cgc tct cta cgc cga aga tcc caa gtt cgc atc gag tgt ccg
 ala OPA pro asp arg glu arg ser leu arg arg arg ser gln val arg ile glu cys pro
 1201/401
 tgg cgg ggg ctt ccg cgc acc gac cgc gcg gcg gcg cct gca ggg cgc ggc gtt gtt cat
 trp arg gly leu pro arg thr asp arg ala ala ala pro ala gly arg gly val val his
 1261/421
 cat cgg tct ggg gat gtt ggt ttc cgg cgt ggc gtt caa aga gac cat gat cgg aag ttt
 his arg ser gly asp val gly phe arg arg gly val gln arg asp his asp arg lys phe
 1321/441
 ccc gat act cag cgt ttt cgg ttt tgt cgt gat gtt cgg tgg tgt ggt gta tgc cat cac
 pro asp thr gln arg phe arg phe cys arg asp val arg trp cys gly val cys his his
 1381/461
 cgg tcc tcg gtt gtc cgg cag gat gga tcg tgg cgg atc ggc tgc tgg ggc ttc gcg cca
 arg ser ser val val arg gln asp gly ser trp arg ile gly cys trp gly phe ala pro
 1441/481
 gcg tcg tac caa ggg ggc cgg ggg ctc att cac cag ccg tat gga aga tc
 ala ser tyr gln gly gly arg gly leu ile his gln pro tyr gly arg

SEQ ID No.45ZC (continued 1)

FIGURE 45ZC (continued 1)

ORF de seq 45ZA directement en fusion avec phoA
 cag tct gtc ggc aag gag gga cgc atg cca ctc tcc gat cat gag cag cgg
 gln ser val gly lys glu gly arg met pro leu ser asp his glu gln arg
 1141/381
 atg ctt gac cag atc gag agc gct ctc tac gcc gaa gat ccc aag ttc gca tcg agt gtc
 met leu asp gln ile glu ser ala leu tyr ala glu asp pro lys phe ala ser ser val
 1201/401
 cgt ggc ggg ggc ttc cgc gca ccg acc gcg cgg cgg cgc ctg cag ggc gcg gcg ttg ttc
 arg gly gly gly phe arg ala pro thr ala arg arg arg leu gln gly ala ala leu phe
 1261/421
 atc atc ggt ctg ggg atg ttg gtt tcc ggc gtg gcg ttc aaa gag acc atg atc gga agt
 ile ile gly leu gly met leu val ser gly val ala phe lys glu thr met ile gly ser
 1321/441
 ttc ccg ata ctc agc gtt ttc ggt ttt gtc gtg atg ttc ggt ggt gtg gtg tat gcc atc
 phe pro ile leu ser val phe gly phe val val met phe gly gly val val tyr ala ile
 1381/461
 acc ggt cct cgg ttg tcc ggc agg atg gat cgt ggc gga tcg gct gct ggg gct tcg cgc
 thr gly pro arg leu ser gly arg met asp arg gly gly ser ala ala gly ala ser arg
 1441/481
 cag cgt cgt acc aag ggg gcc ggg ggc tca ttc acc agc cgt atg gaa gat c
 gln arg arg thr lys gly ala gly gly ser phe thr ser arg met glu asp

SEQ ID No.45A

FIGURE 45A

153/185

Sequence Rv2169c predicted by Cole et al., 1998 (Nature 393:537-544) and containing Seq45A

```

1/1
atg cca ctc tcc gat cat gag cag cgg atg ctt gac cag atc gag agc gct ctc tac gcc
Met pro leu ser asp his glu gln arg met leu asp gln ile glu ser ala leu tyr ala
61/21
gaa gat ccc aag ttc gca tcg agt gtc cgt ggc ggg ggc ttc cgc gca ccg acc gcg cgg
glu asp pro lys phe ala ser ser val arg gly gly gly phe arg ala pro thr ala arg
121/41
cgg cgc ctg cag ggc gcg gcg ttg ttc atc atc ggt ctg ggg atg ttg gtt tcc ggc gtg
arg arg leu gln gly ala ala leu phe ile ile gly leu gly met leu val ser gly val
181/61
gcg ttc aaa gag acc atg atc gga agt ttc ccg ata ctc agc gtt ttc ggt ttt gtc gtg
ala phe lys glu thr met ile gly ser phe pro ile leu ser val phe gly phe val val
241/81
atg ttc ggt ggt gtg gtg tat gcc atc acc ggt cct cgg ttg tcc ggc agg atg gat cgt
met phe gly gly val val tyr ala ile thr gly pro arg leu ser gly arg met asp arg
301/101
ggc gga tcg gct gct ggg gct tcg cgc cag cgt cgt acc aag ggg gcc ggg gcc tca ttc
gly gly ser ala ala gly ala ser arg gln arg arg thr lys gly ala gly gly ser phe
361/121
acc agc cgt atg gaa gat cgg ttc cgg cgc cgc ttc gac gag taa
thr ser arg met glu asp arg phe arg arg phe asp glu OCH

```

SEQ ID No.45D

FIGURE 45D

ORF according to Cole et al., 1998 (Nature 393:537-544) and containing Rv2169c

```

1/1
tga cag tct gtc ggc aag gag gga cgc atg cca ctc tcc gat cat gag cag cgg atg ctt
OPA gln ser val gly lys glu gly arg met pro leu ser asp his glu gln arg met leu
61/21
gac cag atc gag agc gct ctc tac gcc gaa gat ccc aag ttc gca tcg agt gtc cgt ggc
asp gln ile glu ser ala leu tyr ala glu asp pro lys phe ala ser ser val arg gly
121/41
ggg ggc ttc cgc gca ccg acc gcg cgg cgg cgc ctg cag ggc gcg gcg ttg ttc atc atc
gly gly phe arg ala pro thr ala arg arg arg leu gln gly ala ala leu phe ile ile
181/61
ggt ctg ggg atg ttg gtt tcc ggc gtg gcg ttc aaa gag acc atg atc gga agt ttc ccg
gly leu gly met leu val ser gly val ala phe lys glu thr met ile gly ser phe pro
241/81
ata ctc agc gtt ttc ggt ttt gtc gtg atg ttc ggt ggt gtg gtg tat gcc atc acc ggt
ile leu ser val phe gly phe val val met phe gly gly val val tyr ala ile thr gly
301/101
cct cgg ttg tcc ggc agg atg gat cgt ggc gga tcg gct gct ggg gct tcg cgc cag cgt
pro arg leu ser gly arg met asp arg gly gly ser ala ala gly ala ser arg gln arg
361/121
cgt acc aag ggg gcc ggg ggc tca ttc acc agc cgt atg gaa gat cgg ttc cgg cgc cgc
arg thr lys gly ala gly gly ser phe thr ser arg met glu asp arg phe arg arg arg
421/141
ttc gac gag taa
phe asp glu OCH

```

SEQ ID No.45F

FIGURE 45F

1/1											31/11										
cag	ccg	cgc	cgc	atc	gac	cag	ggc	ctc	acg	ccc	ggt	cac	ttc	tcc	gcg	ttc	ctc	aac	aat		
gln	pro	arg	arg	ile	asp	gln	gly	leu	thr	pro	gly	his	phe	ser	ala	phe	leu	asn	asn		
61/21											91/31										
tcc	ggt	gaa	cat	cgc	acc	agg	tta	ggc	agc	aat	ccc	gcg	gac	ccg	cac	ccc	act	cgc	cga		
ser	gly	glu	his	arg	thr	arg	leu	gly	ser	asn	pro	ala	asp	pro	his	pro	thr	arg	arg		
121/41											151/51										
ccg	gcc	aac	tca	cag	aca	ccc	tct	acg	atg	cag	ggt	atg	cgg	acc	ccc	aga	cgc	cac	tgc		
pro	ala	asn	ser	gln	thr	pro	ser	thr	met	gln	gly	met	arg	thr	pro	arg	arg	his	cys		
181/61											211/71										
cgt	cgc	atc	gcc	gtc	ctc	gcc	gcc	gtt	agc	atc	gcc	gcc	act	gtc	gtt	gcc	ggc	tgc	tcg		
arg	arg	ile	ala	val	leu	ala	ala	val	ser	ile	ala	ala	thr	val	val	ala	gly	cys	ser		
241/81											271/91										
tcg	ggc	tcg	aag	cca	agc	ggc	gga	cca	ctt	ccg	gac	gcg	aag	ccg	ctg	gtc	gag	gag	gcc		
ser	gly	ser	lys	pro	ser	gly	gly	pro	leu	pro	asp	ala	lys	pro	leu	val	glu	glu	ala		
301/101											331/111										
acc	gcg	cag	acc	aag	gct	ctc	aag	agc	gcg	cac	atg	gtg	ctg	acg	gtc	aac	ggc	aag	atc		
thr	ala	gln	thr	lys	ala	leu	lys	ser	ala	his	met	val	leu	thr	val	asn	gly	lys	ile		

SEQ ID No.46A

FIGURE 46A

1/1	31/11																		
agc cgc gcc gca tcg acc agg gcc tca cgc	ccg gtc act tct ccg cgt tcc tca aca att																		
ser arg ala ala ser thr arg ala ser arg	pro val thr ser pro arg ser ser thr ile																		
61/21	91/31																		
ccg gtg aac atc gca cca ggt tag gca gca	atc ccg cgg acc cgc acc cca ctc gcc gac																		
pro val asn ile ala pro gly AMB ala ala	ile pro arg thr arg thr pro leu ala asp																		
121/41	151/51																		
cgg cca act cac aga cac cct cta cga tgc	agg gta tgc gga ccc cca gac gcc act gcc																		
arg pro thr his arg his pro leu arg cys	arg val cys gly pro pro asp ala thr ala																		
181/61	211/71																		
gtc gca tcg ccg tcc tcg ccg ccg tta gca	tcg ccg cca ctg tcg ttg ccg gct gct cgt																		
val ala ser pro ser ser pro pro leu ala	ser pro pro leu ser leu pro ala ala arg																		
241/81	271/91																		
cgg gct cga agc caa gcg gcg gac cac ttc	cgg acg cga agc cgc tgg tcg agg agg cca																		
arg ala arg ser gln ala ala asp his phe	arg thr arg ser arg trp ser arg arg pro																		
301/101	331/111																		
ccg cgc aga cca agg ctc tca aga gcg cgc	aca tgg tgc tga cgg tca acg gca aga tc																		
pro arg arg pro arg leu ser arg ala arg	thr trp cys OPA arg ser thr ala arg																		

SEQ ID No. 46B

FIGURE 46B

[illegible]

SEQ ID No. 46C

FIGURE 46C

Coding sequence Rv1411c predicted by Cole et al., 1998 (Nature 393: 537-544) and containing seq46A:

1/1	31/11
atg cgg acc ccc aga cgc cac tgc cgt cgc	atc gcc gtc ctc gcc gcc gtt agc atc gcc
Met arg thr pro arg arg his cys arg arg	ile ala val leu ala ala val ser ile ala
61/21	91/31
gcc act gtc gtt gcc ggc tgc tcg tcg ggc	tcg aag cca agc ggc gga cca ctt ccg gac
ala thr val val ala gly cys ser ser gly	ser lys pro ser gly gly pro leu pro asp
121/41	151/51
gcg aag ccg ctg gtc gag gag gcc acc gcg	cag acc aag gct ctc aag agc gcg cac atg
ala lys pro leu val glu glu ala thr ala	gln thr lys ala leu lys ser ala his met
181/61	211/71
gtg ctg acg gtc aac ggc aag atc ccg gga	ctg tct ctg aag acg ctg agc ggc gat ctc
val leu thr val asn gly lys ile pro gly	leu ser leu lys thr leu ser gly asp leu
241/81	271/91
acc acc aac ccc acc gcc gcg acg gga aac	gtc aag ctc acg ctg ggt ggg tct gat atc
thr thr asn pro thr ala ala thr gly asn	val lys leu thr leu gly gly ser asp ile
301/101	331/111
gat gcc gac ttc gtg gtg ttc gac ggg atc	ctg tac gcc acc ctg acg ccc aac cag tgg
asp ala asp phe val val phe asp gly ile	leu tyr ala thr leu thr pro asn gln trp
361/121	391/131
agc gat ttc ggt ccc gcc gcc gac atc tac	gac ccc gcc cag gtg ctg aat ccg gat acc
ser asp phe gly pro ala ala asp ile tyr	asp pro ala gln val leu asn pro asp thr
421/141	451/151
ggc ctg gcc aac gtg ctg gcg aat ttc gcc	gac gca aaa gcc gaa ggg cgg gat acc atc
gly leu ala asn val leu ala asn phe ala	asp ala lys ala glu gly arg asp thr ile
481/161	511/171
aac ggc cag aac acc atc cgc atc agc ggg	aag gta tcg gca cag gcg gtg aac cag ata
asn gly gln asn thr ile arg ile ser gly	lys val ser ala gln ala val asn gln ile
541/181	571/191
gcg ccg ccg ttc aac gcg acg cag ccg gtg	ccg gcg acc gtc tgg att cag gag acc ggc
ala pro pro phe asn ala thr gln pro val	pro ala thr val trp ile gln glu thr gly
601/201	631/211
gat cat caa ctg gca cag gcc cag ttg gac	cgc ggc tcg ggc aat tcc gtc cag atg acc
asp his gln leu ala gln ala gln leu asp	arg gly ser gly asn ser val gln met thr
661/221	691/231
ttg tcg aaa tgg ggc gag aag gtc cag gtc	acg aag ccc ccg gtg agc tga
leu ser lys trp gly glu lys val gln val	thr lys pro pro val ser OPA

SEQ ID No.46D

FIGURE 46D

157/185

ORF according to Cole et al., 1998 (Nature 393: 537-544):
and containing the coding sequence Rv1411c:

1/1	31/11
tag ctc acc cag gtt gga ccg gtt cag tgt	ctc ggc cat cac gtc ggc ggt gaa ttg gcc
AMB leu thr gln val gly pro val gln cys	leu gly his his val gly gly glu leu ala
61/21	91/31
gtc ggg caa tac atc gac gac cgt cag aca	cac gcc gtt gac agc gat cga gtc gcc gtg
val gly gln tyr ile asp asp arg gln thr	his ala val asp ser asp arg val ala val
121/41	151/51
gcc ggc gtc ggc ggt aac cat cgg acc gcg	gat ggt cag ccg cgc cgc atc gac cag ggc
ala gly val gly gly asn his arg thr ala	asp gly gln pro arg arg ile asp gln gly
181/61	211/71
ctc acg ccc ggt cac ttc tcc gcg ttc ctc	aac aat tcc ggt gaa cat cgc acc agg tta
leu thr pro gly his phe ser ala phe leu	asn asn ser gly glu his arg thr arg leu
241/81	271/91
ggc agc aat ccc gcg gac ccg cac ccc act	cgc cga ccg gcc aac tca cag aca ccc tct
gly ser asn pro ala asp pro his pro thr	arg arg pro ala asn ser gln thr pro ser
301/101	331/111
acg atg cag ggt atg cgg acc ccc aga cgc	cac tgc cgt cgc atc gcc gtc ctc gcc gcc
thr met gln gly met arg thr pro arg arg	his cys arg arg ile ala val leu ala ala
361/121	391/131
gtt agc atc gcc gcc act gtc gtt gcc ggc	tgc tcg tcg ggc tcg aag cca agc ggc gga
val ser ile ala ala thr val val ala gly	cys ser ser gly ser lys pro ser gly gly
421/141	451/151
cca ctt ccg gac gcg aag ccg ctg gtc gag	gag gcc acc gcg cag acc aag gct ctc aag
pro leu pro asp ala lys pro leu val glu	glu ala thr ala gln thr lys ala leu lys
481/161	511/171
agc gcg cac atg gtg ctg acg gtc aac ggc	aag atc ccg gga ctg tct ctg aag acg ctg
ser ala his met val leu thr val asn gly	lys ile pro gly leu ser leu lys thr leu
541/181	571/191
agc ggc gat ctc acc acc aac ccc acc gcc	gcg acg gga aac gtc aag ctc acg ctg ggt
ser gly asp leu thr thr asn pro thr ala	ala thr gly asn val lys leu thr leu gly
601/201	631/211
ggg tct gat atc gat gcc gac ttc gtg gtg	ttc gac ggg atc ctg tac gcc acc ctg acg
gly ser asp ile asp ala asp phe val val	phe asp gly ile leu tyr ala thr leu thr
661/221	691/231
ccc aac cag tgg agc gat ttc ggt ccc gcc	gcc gac atc tac gac ccc gcc cag gtg ctg
pro asn gln trp ser asp phe gly pro ala	ala asp ile tyr asp pro ala gln val leu
721/241	751/251
aat ccg gat acc ggc ctg gcc aac gtg ctg	gcg aat ttc gcc gac gca aaa gcc gaa ggg
asn pro asp thr gly leu ala asn val leu	ala asn phe ala asp ala lys ala glu gly
781/261	811/271
cgg gat acc atc aac ggc cag aac acc atc	cgc atc agc ggg aag gta tcg gca cag gcg
arg asp thr ile asn gly gln asn thr ile	arg ile ser gly lys val ser ala gln ala
841/281	871/291
gtg aac cag ata gcg ccg ccg ttc aac gcg	acg cag ccg gtg ccg gcg acc gtc tgg att
val asn gln ile ala pro pro phe asn ala	thr gln pro val pro ala thr val trp ile
901/301	931/311
cag gag acc ggc gat cat caa ctg gca cag	gcc cag ttg gac cgc ggc tcg gcc aat tcc
gln glu thr gly asp his gln leu ala gln	ala gln leu asp arg gly ser gly asn ser
961/321	991/331
gtc cag atg acc ttg tcg aaa tgg ggc gag	aag gtc cag gtc acg aag ccc ccg gtg agc
val gln met thr leu ser lys trp gly glu	lys val gln val thr lys pro pro val ser
1021/341	
tga	
OPA	

SEQ ID No.46F

FIGURE 46F

158/185

1/1 31/11
gag ctg gtc aac ggc gcc ggc atc gac gac gcc gcc gtc gtg acc tgc cgg ccg gac agc
glu leu val asn gly ala gly ile asp asp ala ala val val thr cys arg pro asp ser
61/21 91/31
ctg gcc gat gcc cag cag atg gtc gag gcg gca ctg ggc cga tat ggc cgt ttg gac gga
leu ala asp ala gln gln met val glu ala ala leu gly arg tyr gly arg leu asp gly
121/41 151/51
gtg ttg gtg gcc tcg ggc agc aac cat gtg gcg ccc att acc gag atg gcc gtc gag gac
val leu val ala ser gly ser asn his val ala pro ile thr glu met ala val glu asp
181/61 211/71
ttc gac gct gtg atg gac gcg aac gtg cgg ggt gcc tgg ctg gtg tgt cgg gcg gcc gga
phe asp ala val met asp ala asn val arg gly ala trp leu val cys arg ala ala gly
241/81 271/91
cgg gtg ctg ctc gag cag ggt cag ggc gcc agc gtg gtg ctg gtg tcg tcc gtt cgc gcc
arg val leu leu glu gln gly gln gly gly ser val val leu val ser ser val arg gly
301/101 331/111
ggg ttg ggc aat gcc gcc ggt tac agc gcg tac tgc ccg tcg aag gcg gcc acc gat c
gly leu gly asn ala ala gly tyr ser ala tyr cys pro ser lys ala gly thr asp

SEQ ID No.47A

FIGURE 47A

1/1 31/11
agc tgg tca acg gcg ccg gca tcg acg acg ccg ccg tcg tga cct gcc ggc cgg aca gcc
ser trp ser thr ala pro ala ser thr thr pro pro ser OPA pro ala gly arg thr ala
61/21 91/31
tgg ccg atg ccc agc aga tgg tcg agg ccg cac tgg gcc gat atg gcc gtt tgg acg gag
trp pro met pro ser arg trp ser arg arg his trp ala asp met ala val trp thr glu
121/41 151/51
tgt tgg tgg cct cgg gca gca acc atg tgg cgc cca tta ccg aga tgg ccg tcg agg act
cys trp trp pro arg ala ala thr met trp arg pro leu pro arg trp pro ser arg thr
181/61 211/71
tcg acg ctg tga tgg acg cga acg tgc ggg gtg cct gcc tgg tgt gtc ggg ccg ccg gac
ser thr leu OPA trp thr arg thr cys gly val pro gly trp cys val gly arg pro asp
241/81 271/91
ggg tgc tgc tcg agc agg gtc agg gcg gca gcg tgg tgc tgg tgt cgt ccg ttc gcg gcg
gly cys cys ser ser arg val arg ala ala ala trp cys trp cys arg pro phe ala ala
301/101 331/111
ggt tgg gca atg ccg ccg gtt aca gcg cgt act gcc cgt cga agg ccg gca ccg atc
gly trp ala met pro pro val thr ala arg thr ala arg arg arg ala pro ile

SEQ ID No.47B

FIGURE 47B

SEE A CURRENT SHEET WITH E 26

160/185

Coding sequence Rv1714 predicted by Cole et al., 1998 (Nature 393: 537-544) and containing seq 47A:

1/1	31/11
gtg gag gaa atg gcg ctg gct cag cag gtg	ccg aac ctg ggt ctg gcg cgc ttc agc gtg
val glu glu met ala leu ala gln gln val	pro asn leu gly leu ala arg phe ser val
61/21	91/31
cag gac aag tcg atc ctg atc acc ggc gcg	acc ggt tcg ttg ggc cga gtt gcc gcc cgg
gln asp lys ser ile leu ile thr gly ala	thr gly ser leu gly arg val ala ala arg
121/41	151/51
gcg ctg gcc gac gcg gga gcg cgg ctg aca	ctg gcc ggc ggc aac tcg gcc ggt ctg gcc
ala leu ala asp ala gly ala arg leu thr	leu ala gly gly asn ser ala gly leu ala
181/61	211/71
gag ctg gtc aac ggc gcc ggc atc gac gac	gcc gcc gtc gtg acc tgc cgg ccg gac agc
glu leu val asn gly ala gly ile asp asp	ala ala val val thr cys arg pro asp ser
241/81	271/91
ctg gcc gat gcc cag cag atg gtc gag gcg	gca ctg ggc cga tat ggc cgt ttg gac gga
leu ala asp ala gln gln met val glu ala	ala leu gly arg tyr gly arg leu asp gly
301/101	331/111
gtg ttg gtg gcc tcg ggc agc aac cat gtg	gcg ccc att acc gag atg gcc gtc gag gac
val leu val ala ser gly ser asn his val	ala pro ile thr glu met ala val glu asp
361/121	391/131
ttc gac gct gtg atg gac gcg aac gtg cgg	ggt gcc tgg ctg gtg tgt cgg gcg gcc gga
phe asp ala val met asp ala asn val arg	gly ala trp leu val cys arg ala ala gly
421/141	451/151
cgg gtg ctg ctc gag cag ggt cag ggc ggc	agc gtg gtg ctg gtg tcg tcc gtt cgc gcc
arg val leu leu glu gln gly gln gly gly	ser val val leu val ser ser val arg gly
481/161	511/171
ggg ttg ggc aat gcc gcc ggt tac agc gcg	tac tgc ccg tcg aag gcg ggc acc gat ctg
gly leu gly asn ala ala gly tyr ser ala	tyr cys pro ser lys ala gly thr asp leu
541/181	571/191
ttg gcc aag aca ttg gcg gcc gaa tgg ggc	ggt cac ggc att cgg gtg aac gcg ctg gcg
leu ala lys thr leu ala ala glu trp gly	gly his gly ile arg val asn ala leu ala
601/201	631/211
ccg acg gtg ttt cgg tcc gcg gtg acc gag	tgg atg ttc acc gac gat ccg aag ggc cgg
pro thr val phe arg ser ala val thr glu	trp met phe thr asp asp pro lys gly arg
661/221	691/231
gcc acc cgg gag gcg atg ctc gcc cgg atc	ccg ttg cgc cgc ttc gcc gaa ccg gaa gac
ala thr arg glu ala met leu ala arg ile	pro leu arg arg phe ala glu pro glu asp
721/241	751/251
ttc gtc ggc gcc ctg atc tat ctg ctc agc	gac gcc tcg agc ttc tac acc ggc cag gtg
phe val gly ala leu ile tyr leu leu ser	asp ala ser ser phe tyr thr gly gln val
781/261	811/271
atg tat ctg gac ggc ggg tac acc gca tgc tga	
met tyr leu asp gly gly tyr thr ala cys OPA	

SEQ ID No.47D

FIGURE 47D

161/185

ORF according to Cole et al., 1998 (Nature 393: 537-544) and containing the coding sequence Rv1714:

24/1	54/11
tag gtg gag gaa atg gcg ctg gct cag cag	gtg ccg aac ctg ggt ctg gcg cgc ttc agc
AMB val glu glu met ala leu ala gln gln	val pro asn leu gly leu ala arg phe ser
84/21	114/31
gtg cag gac aag tcg atc ctg atc acc ggc	gcg acc ggt tcg ttg ggc cga gtt gcc gcc
val gln asp lys ser ile leu ile thr gly	ala thr gly ser leu gly arg val ala ala
144/41	174/51
cgg gcg ctg gcc gac gcg gga gcg cgg ctg	aca ctg gcc ggc ggc aac tcg gcc ggt ctg
arg ala leu ala asp ala gly ala arg leu	thr leu ala gly gly asn ser ala gly leu
204/61	234/71
gcc gag ctg gtc aac ggc gcc ggc atc gac	gac gcc gcc gtc gtg acc tgc cgg ccg gac
ala glu leu val asn gly ala gly ile asp	asp ala ala val val thr cys arg pro asp
264/81	294/91
agc ctg gcc gat gcc cag cag atg gtc gag	gcg gca ctg ggc cga tat ggc cgt ttg gac
ser leu ala asp ala gln gln met val glu	ala ala leu gly arg tyr gly arg leu asp
324/101	354/111
gga gtg ttg gtg gcc tcg ggc agc aac cat	gtg gcg ccc att acc gag atg gcc gtc gag
gly val leu val ala ser gly ser asn his	val ala pro ile thr glu met ala val glu
384/121	414/131
gac ttc gac gct gtg atg gac gcg aac gtg	cgg ggt gcc tgg ctg gtg tgt cgg gcg gcc
asp phe asp ala val met asp ala asn val	arg gly ala trp leu val cys arg ala ala
444/141	474/151
gga cgg gtg ctg ctc gag cag ggt cag ggc	ggc agc gtg gtg ctg gtg tcg tcc gtt cgc
gly arg val leu leu glu gln gly gln gly	gly ser val val leu val ser ser val arg
504/161	534/171
ggc ggg ttg ggc aat gcc gcc ggt tac agc	gcg tac tgc ccg tcg aag gcg ggc acc gat
gly gly leu gly asn ala ala gly tyr ser	ala tyr cys pro ser lys ala gly thr asp
564/181	594/191
ctg ttg gcc aag aca ttg gcg gcc gaa tgg	ggc ggt cac ggc att cgg gtg aac gcg ctg
leu leu ala lys thr leu ala ala glu trp	gly gly his gly ile arg val asn ala leu
624/201	654/211
gcg ccg acg gtg ttt cgg tcc gcg gtg acc	gag tgg atg ttc acc gac gat ccg aag ggc
ala pro thr val phe arg ser ala val thr	glu trp met phe thr asp asp pro lys gly
684/221	714/231
cgg gcc acc cgg gag gcg atg ctc gcc cgg	atc ccg ttg cgc cgc ttc gcc gaa ccg gaa
arg ala thr arg glu ala met leu ala arg	ile pro leu arg arg phe ala glu pro glu
744/241	774/251
gac ttc gtc ggc gcc ctg atc tat ctg ctc	agc gac gcc tcg agc ttc tac acc ggc cag
asp phe val gly ala leu ile tyr leu leu	ser asp ala ser ser phe tyr thr gly gln
804/261	834/271
gtg atg tat ctg gac ggc ggg tac acc gca	tgc tga
val met tyr leu asp gly gly tyr thr ala	cys OPA

SEQ ID No.47F

FIGURE 47F

Abstract

FIGURE 48A

Abstract

FIGURE 48B

Abstract

FIGURE 48C

Coding sequence Rv0331 predicted by Cole et al., 1998 (Nature 393: 537-544) and containing seq48A:

```

1/1
atg agc aag acg gtt ctc atc ctt ggc ggc ggt gtc ggc ggc ctg acc acc gcc gac acc
Met ser lys thr val leu ile leu gly ala gly val gly gly leu thr thr ala asp thr
61/21
ctc cgt caa ctg cta cca cct gag gat cga atc ata ttg gtg gac agg agc ttt gac ggg
leu arg gln leu leu pro pro glu asp arg ile ile leu val asp arg ser phe asp gly
121/41
acg ctg ggc ttg tcg ttg cta tgg gtg ttg cgg ggc tgg cgg cgt gac gac gtc cgc
thr leu gly leu ser leu leu trp val leu arg gly trp arg arg pro asp asp val arg
181/61
gtc cgc ccc acc gcg gcg tcg ctg ccc ggt gtg gaa atg gtt act gca acc gtc gcc cac
val arg pro thr ala ala ser leu pro gly val glu met val thr ala thr val ala his
241/81
att gac atc gcg gcc cag gta gtg cac acc gac aac agc gtc atc ggc tat gac gcg ttg
ile asp ile ala ala gln val val his thr asp asn ser val ile gly tyr asp ala leu
301/101
gtg atc gca tta ggt gcg gcg ctg aac acc gac gcc gtt ccc gga ctg tcg gac gcg ctc
val ile ala leu gly ala ala leu asn thr asp ala val pro gly leu ser asp ala leu
361/121
gac gcc gac gtc gcg ggc cag ttc tac acc ctg gac ggc gcg gct gag ctg cgt gcg aag
asp ala asp val ala gly gln phe tyr thr leu asp gly ala ala glu leu arg ala lys
421/141
gtc gag gcg ctc gag cat ggc cgg atc gct gtg gct atc gcc ggg gtg ccg ttc aaa tgc
val glu ala leu glu his gly arg ile ala val ala ile ala gly val pro phe lys cys
481/161
cca gcc gca ccg ttc gaa gcg gcg ttt ctg atc gcc gcc caa ctc ggt gac cgc tac gcc
pro ala ala pro phe glu ala ala phe leu ile ala ala gln leu gly asp arg tyr ala
541/181
acc gga acc gta cag atc gac acg ttc acg cct gac ccg ctg ccg atg ccc gtt gca ggt
thr gly thr val gln ile asp thr phe thr pro asp pro leu pro met pro val ala gly
601/201
ccc gag gtc ggc gag gct ttg gtc tcg atg ctc aag gat cac ggt gtc ggc ttc cat cct
pro glu val gly glu ala leu val ser met leu lys asp his gly val gly phe his pro
661/221
cgc aag gcc cta gct cgc gtc gat gag gcc gca agg acg atg cac ttc ggt gac ggc acg
arg lys ala leu ala arg val asp glu ala ala arg thr met his phe gly asp gly thr
721/241
tcc gaa ccg ttc gat ctg ctt gcc gtg gtc ccc ccg cac gtg ccc tcc gcc gcg gcg ccg
ser glu pro phe asp leu leu ala val val pro pro his val pro ser ala ala ala arg
781/261
tca gcg ggt ctc agc gaa tcc ggg tgg ata ccc gtg gac ccg cgc acc ctg tcc act agc
ser ala gly leu ser glu ser gly trp ile pro val asp pro arg thr leu ser thr ser
841/281
gcc gac aac gtg tgg gcc atc ggc gat gcg acc gtg ctg acg ctg ccg aat ggc aaa ccg
ala asp asn val trp ala ile gly asp ala thr val leu thr leu pro asn gly lys pro
901/301
ctg ccc aag gct gcc gtg ttc gcc gaa gcc cag gcc gca gtt gtc gcc cac ggc gtc gcc
leu pro lys ala ala val phe ala glu ala gln ala ala val val ala his gly val ala
961/321
cgc cat ctc ggt tac gac gta gct gag cgc cac ttc acc ggc acg ggc gcc tgc tac gtc
arg his leu gly tyr asp val ala glu arg his phe thr gly thr gly ala cys tyr val
1021/341
gag acc ggt gat cac cag gca gcc aag ggc gac ggc gat ttc ttc gct ccg tcg gcg ccc
glu thr gly asp his gln ala ala lys gly asp gly asp phe phe ala pro ser ala pro
1081/361
tcg gtg acg ctg tac ccg ccg tcg ccg gag ttt cac gag gag aag gtc gca caa gaa ctg
ser val thr leu tyr pro pro ser arg glu phe his glu glu lys val ala gln glu leu
1141/381
gcc tgg ctg acc cgc tgg aag acg tga
ala trp leu thr arg trp lys thr OPA

```

SEQ ID No.48D

FIGURE 48D

ORF according to Cole et al., 1998 (Nature 393: 537-544) and containing coding sequence Rv0331:

```

1/1                                31/11
tga aca ccc gcg ccg acg cgg cga caa tcg cgg aaa acc ggt ccg ccg gaa tgc tgc ggg
OPA thr pro ala pro thr arg arg gln ser arg lys thr gly pro arg glu cys cys gly
61/21                                91/31
cca tgg gcc gat aat agt ttg act gac tcg gtc agt cac ccc aag acc ttg cgc aag act
pro trp ala asp asn ser leu thr asp ser val ser his pro lys thr leu arg lys thr
121/41                                151/51
gcg gcg gaa tct aat att cca aag ata tat gga act cga tgc gaa gga atc agg ctc atg
ala ala glu ser asn ile pro lys ile tyr gly thr arg cys glu gly ile arg leu met
181/61                                211/71
agc aag acg gtt ctc atc ctt ggc gcg ggt gtc ggc ggc ctg acc acc gcc gac acc ctc
ser lys thr val leu ile leu gly ala gly val gly gly leu thr thr ala asp thr leu
241/81                                271/91
cgt caa ctg cta cca cct gag gat cga atc ata ttg ttg gac agg agc ttt gac ggg acg
arg gln leu leu pro pro glu asp arg ile ile leu val asp arg ser phe asp gly thr
301/101                               331/111
ctg ggc ttg tcg ttg cta tgg gtg ttg cgg ggc ttg ccg ccg cct gac gac gtc cgc gtc
leu gly leu ser leu leu trp val leu arg gly trp arg arg pro asp asp val arg val
361/121                               391/131
cgc ccc acc gcg gcg tcg ctg ccc ggt gtg gaa atg gtt act gca acc gtc gcc cac att
arg pro thr ala ala ser leu pro gly val glu met val thr ala thr val ala his ile
421/141                               451/151
gac atc gcg gcc cag gta gtg cac acc gac aac agc gtc atc ggc tat gac gcg ttg gtg
asp ile ala ala gln val val his thr asp asn ser val ile gly tyr asp ala leu val
481/161                               511/171
atc gca tta ggt gcg gcg ctg aac acc gac gcc gtt ccc gga ctg tcg gac gcg ctc gac
ile ala leu gly ala ala leu asn thr asp ala val pro gly leu ser asp ala leu asp
541/181                               571/191
gcc gac gtc gcg ggc cag ttc tac acc ctg gac ggc gcg gct gag ctg cgt gcg aag gtc
ala asp val ala gly gln phe tyr thr leu asp gly ala ala glu leu arg ala lys val
601/201                               631/211
gag gcg ctc gag cat ggc ccg atc gct gtg gct atc gcc ggg gtg ccg ttc aaa tgc cca
glu ala leu glu his gly arg ile ala val ala ile ala gly val pro phe lys cys pro
661/221                               691/231
gcc gca ccg ttc gaa gcg gcg ttt ctg atc gcc gcc caa ctc ggt gac cgc tac gcc acc
ala ala pro phe glu ala ala phe leu ile ala ala gln leu gly asp arg tyr ala thr
721/241                               751/251
gga acc gta cag atc gac acg ttc acg cct gac ccg ctg ccg atg ccc gtt gca ggt ccc
gly thr val gln ile asp thr phe thr pro asp pro leu pro met pro val ala gly pro
781/261                               811/271
gag gtc ggc gag gct ttg gtc tcg atg ctc aag gat cac ggt gtc ggc ttc cat cct cgc
glu val gly glu ala leu val ser met leu lys asp his gly val gly phe his pro arg
841/281                               871/291
aag gcc cta gct cgc gtc gat gag gcc gca agg acg atg cac ttc ggt gac ggc acg tcc
lys ala leu ala arg val asp glu ala ala arg thr met his phe gly asp gly thr ser

```

SEQ ID No.48F

FIGURE 48F

901/301
 gaa ccg ttc gat ctg ctt gcc gtg gtc ccc ccg cac gtg ccc tcc gcc gcg gcg cgg tca
 glu pro phe asp leu leu ala val val pro pro his val pro ser ala ala ala arg ser
 961/321
 gcg ggt ctc agc gaa tcc ggg tgg ata ccc gtg gac ccg cgc acc ctg tcc act agc gcc
 ala gly leu ser glu ser gly trp ile pro val asp pro arg thr leu ser thr ser ala
 1021/341
 gac aac gtg tgg gcc atc ggc gat gcg acc gtg ctg acg ctg ccg aat ggc aaa ccg ctg
 asp asn val trp ala ile gly asp ala thr val leu thr leu pro asn gly lys pro leu
 1081/361
 ccc aag gct gcc gtg ttc gcc gaa gcc cag gcc gca gtt gtc gcc cac ggc gtc gcc cgc
 pro lys ala ala val phe ala glu ala gln ala ala val val ala his gly val ala arg
 1141/381
 cat ctc ggt tac gac gta gct gag cgc cac ttc acc ggc acg ggc gcc tgc tac gtc gag
 his leu gly tyr asp val ala glu arg his phe thr gly thr gly ala cys tyr val glu
 1201/401
 acc ggt gat cac cag gca gcc aag ggc gac ggc gat ttc ttc gct ccg tcg gcg ccc tcg
 thr gly asp his gln ala ala lys gly asp gly asp phe phe ala pro ser ala pro ser
 1261/421
 gtg acg ctg tac ccg ccg tcg cgg gag ttt cac gag gag aag gtc gca caa gaa ctg gcc
 val thr leu tyr pro pro ser arg glu phe his glu glu lys val ala gln glu leu ala
 1321/441
 tgg ctg acc cgc tgg aag acg tga
 trp leu thr arg trp lys thr OPA

SEQ ID No.48F (continued)

FIGURE 48F (continued)

Fragment amplified by PCR based on the sequence similarities with a serine protease of the E.coli htrA family (creation of the BamHI site at the 5' end and of the SnaBI site at the 3' end) and subcloned into the vector pJVED:

```

1/1                               31/11
cca tct aca ccg ctc aac agc cgg gcc aga cgc tgc cgg tcg gtg ctg ccg aga agg cgg
pro ser thr pro leu asn ser arg ala arg arg cys arg ser val leu pro arg arg arg
61/21                               91/31
tga tcc gtg gcg agt tgt tca tgt cgc ggc gca cca ccg ccg acc aac ggg tgc ttg cca
OPA ser val ala ser cys ser cys arg gly ala pro pro pro thr asn gly cys leu pro
121/41                               151/51
tcc gtc tga cca acg gta gtt cgc tgc tga tct cca aaa gtc tca agc cca ccg aag cag
ser val OPA pro thr val val arg cys OPA ser pro lys val ser ser pro pro lys gln
181/61                               211/71
tca tga aca agc tgc gtt ggg tgc tat tga tcg tgg gtg gga tcg ggg tgg cgg tcg ccg
ser OPA thr ser cys val gly cys tyr OPA ser trp val gly ser gly trp arg ser pro
241/81                               271/91
cgg tgg ccg ggg gga tgg tca ccc ggg ccg ggc tga ggc cgg tgg gcc gcc tca ccg aag
arg trp pro gly gly trp ser pro gly pro gly OPA gly arg trp ala ala ser pro lys
301/101                               331/111
cgg ccg agc ggg tgg cgc gaa ccg acg acc tgc ggc cca tcc ccg tct tcg gca gcg acg
arg pro ser gly trp arg glu pro thr thr cys gly pro ser pro ser ser ala ala thr
361/121                               391/131
aat tgg cca ggc tga cag agg cat tca att taa tgc tgc ggg cgc tgg ccg agt cac ggg
asn trp pro gly OPA gln arg his ser ile OCH cys cys gly arg trp pro ser his gly
421/141                               451/151
aac ggc agg caa ggc tgg tta ccg acg ccg gac atg aat tgc gta ccc cgc taa cgt cgc
asn gly arg gln gly trp leu pro thr pro asp met asn cys val pro arg OCH arg arg
481/161                               511/171
tgc gca cca atg tcg aac tct tga tgg cct cga tgg ccc ccg ggg ctc cgc ggc tac cca
cys ala pro met ser asn ser OPA trp pro arg trp pro arg gly leu arg gly tyr pro
541/181                               571/191
agc agg aga tgg tcg acc tgc gtg ccg atg tgc tgg ctc aaa tcg agg aat tgt cca cac
ser arg arg trp ser thr cys val pro met cys trp leu lys ser arg asn cys pro his
601/201                               631/211
tgg tag gcg att tgg tgg acc tgt ccc gag gcg acg ccg gag aag tgg tgc acg agc cgg
trp AMB ala ile trp trp thr cys pro glu ala thr pro glu lys trp cys thr ser arg
661/221                               691/231
tcg aca tgg ctg acg tcg tcg acc gca gcc tgg agc ggg tca ggc ggc ggc gca acg ata
ser thr trp leu thr ser ser thr ala ala trp ser gly ser gly gly gly ala thr ile
721/241                               751/251
tcc ttt tcg acg tcg agg tga ttg ggt ggc agg ttt atg gcg ata ccg ctg gat tgt cgc
ser phe ser thr ser arg OPA leu gly gly arg phe met ala ile pro leu asp cys arg
781/261                               811/271
gga tgg cgc tta acc tga tgg aca acg ccg cga agt gga gcc cgc ccg gcg gcc acg tgg
gly trp arg leu thr OPA trp thr thr pro arg ser gly ala arg arg ala ala thr trp
841/281                               871/291
gtg tca ggc tga gcc agc tcg acg cgt cgc acg ctg agc tgg tgg ttt ccg acc gcg gcc
val ser gly OPA ala ser ser thr arg arg thr leu ser trp trp phe pro thr ala ala

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SEQ ID No.49A

FIGURE 49A

901/301
 cgg gca ttc ccg tgc agg agc gcc gtc tgg tgt ttg aac ggt ttt acc ggt cgg cat cgg
 arg ala phe pro cys arg ser ala val trp cys leu asn gly phe thr gly arg his arg
 961/321
 cac ggg cgt tgc cgg gtt cgg gcc tcg ggt tgg cga tcg tca aac agg tgg tgc tca acc
 his gly arg cys arg val arg ala ser gly trp arg ser ser asn arg trp cys ser thr
 1021/341
 acg gcg gat tgc tgc gca tcg aag aca ccg acc cag gcg gcc agc ccc ctg gaa cgt cga
 thr ala asp cys cys ala ser lys thr pro thr gln ala ala ser pro leu glu arg arg
 1081/361
 ttt acg tgc tgc tcc ccg gcc gtc gga tgc cga ttc cgc agc ttc ccg gtg cga cgg ctg
 phe thr cys cys ser pro ala val gly cys arg phe arg ser phe pro val arg arg leu
 1141/381
 gcg ctc gga gca cgg aca tcg aga act ctc ggg gtt cgg cga acg tta tct cag tgg aat
 ala leu gly ala arg thr ser arg thr leu gly val arg arg thr leu ser gln trp asn
 1201/401
 ctc agt cca cgc gcg caa cct agt tgt gca gtt act gtt gaa agc cac acc cat gcc agt
 leu ser pro arg ala gln pro ser cys ala val thr val glu ser his thr his ala ser
 1261/421
 cca cgc atg gcc aag ttg gcc cga gta gtg ggc cta gta cag gaa gag caa cct agc gac
 pro arg met ala lys leu ala arg val val gly leu val gln glu glu gln pro ser asp
 1321/441
 atg acg aat cac cca cgg tat tcg cca ccg ccg cag cag ccg gga acc cca ggt tat gct
 met thr asn his pro arg tyr ser pro pro pro gln gln pro gly thr pro gly tyr ala
 1381/461
 cag ggg cag cag caa acg tac agc cag cag ttc gac tgg cgt tac cca ccg tcc ccg ccc
 gln gly gln gln gln thr tyr ser gln gln phe asp trp arg tyr pro pro ser pro pro
 1441/481
 ccg cag cca acc cag tac cgt caa ccc tac gag gcg ttg ggt ggt acc cgg ccg ggt ctg
 pro gln pro thr gln tyr arg gln pro tyr glu ala leu gly gly thr arg pro gly leu
 1501/501
 ata cct ggc gtg att ccg acc atg acg ccc cct cct ggg atg gtt cgc caa cgc cct cgt
 ile pro gly val ile pro thr met thr pro pro pro gly met val arg gln arg pro arg
 1561/521
 gca ggc atg ttg gcc atc ggc gcg gtg acg ata gcg gtg gtg tcc gcc ggc atc ggc ggc
 ala gly met leu ala ile gly ala val thr ile ala val val ser ala gly ile gly gly
 1621/541
 gcg gcc gca tcc ctg gtc ggg ttc aac ccg gca ccc gcc ggc ccc agc ggc ggc cca gtg
 ala ala ala ser leu val gly phe asn arg ala pro ala gly pro ser gly gly pro val
 1681/561
 gct gcc agc gcg gcg cca agc atc ccc gca gca aac atg ccg ccg ggg tcg gtc gaa cag
 ala ala ser ala ala pro ser ile pro ala ala asn met pro pro gly ser val glu gln
 1741/581
 gtg gcg gcc aag gtg gtg ccc agt gtc gtc atg ttg gaa acc gat ctg ggc cgc cag tcg
 val ala ala lys val val pro ser val val met leu glu thr asp leu gly arg gln ser
 1801/601
 gag gag ggc tcc ggc atc att ctg tct gcc gag ggg ctg atc ttg acc aac aac cac gtg
 glu glu gly ser gly ile ile leu ser ala glu gly leu ile leu thr asn asn his val
 1861/621
 atc gcg gcg gcc gcc aag cct ccc ctg ggc agt ccg ccg ccg aaa acg acg gta
 ile ala ala ala ala lys pro pro leu gly ser pro pro pro lys thr thr val

SEQ ID No.49A (continued 1)

FIGURE 49A (continued 1)

1/1	cat cta cac cgc tca aca gcc ggg cca gac	31/11	gct gcc ggt cgg tgc tgc cga gaa ggc ggt
his leu his arg ser thr ala gly pro asp	61/21	gat ccg tgg cga gtt gtt cat gtc gcg gcg	91/31
asp pro trp arg val val his val ala ala	121/41	ccg tct gac caa cgg tag ttc gct gct gat	151/51
pro ser asp gln arg AMB phe ala ala asp	181/61	cat gaa caa gct gcg ttg ggt gct att gat	211/71
his glu gln ala ala leu gly ala ile asp	241/81	ggg ggc cgg ggg gat ggt cac ccg ggc cgg	271/91
gly gly arg gly asp gly his pro gly arg	301/101	ggc cga gcg ggt ggc gcg aac cga cga cct	331/111
gly arg ala gly gly ala asn arg arg pro	361/121	att ggc cag gct gac aga ggc att caa ttt	391/131
ile gly gln ala asp arg gly ile gln phe	421/141	acg gca ggc aag gct ggt tac cga cgc cgg	451/151
thr ala gly lys ala gly tyr arg arg arg	481/161	gcg cac caa tgt cga act ctt gat ggc ctc	511/171
ala his gln cys arg thr leu asp gly leu	541/181	gca gga gat ggt cga cct gcg tgc cga tgt	571/191
ala gly asp gly arg pro ala cys arg cys	601/201	ggg ggc gct taa cct gat gga caa cgc cgc	631/211
asp gly ala OCH pro asp gly gln arg arg	661/221	cga cat ggc tga cgt cgt cga ccg cag cct	691/231
cga cat ggc tga cgt cgt cga ccg cag cct	721/241	cct ttt cga cgt cga ggt gat tgg gtg gca	751/251
pro phe arg arg arg gly asp trp val ala	781/261	gat ggc gct taa cct gat gga caa cgc cgc	811/271
gat ggc gct taa cct gat gga caa cgc cgc	841/281	tgt cag gct gag cca gct cga cgc gtc gca	871/291
asp gly ala OCH pro asp gly gln arg arg	901/301	cys gln ala glu pro ala arg arg val ala	931/311
ggg cat tcc cgt gca gga gcg ccg tct ggt	961/321	acg ggc gtt gcc ggg ttc ggg cct cgg gtt	991/331
gly his ser arg ala gly ala pro ser gly	1021/341	thr gly val ala gly phe gly pro arg val	1051/351
cgg cgg att gct gcg cat cga aga cac cga		arg arg ile ala ala his arg arg his arg	

SEQ ID No.49B

FIGURE 49B

1081/361
 tta cgt gct gct ccc cgg ccg tcg gat gcc gat tcc gca gct tcc cgg tgc gac ggc tgg
 leu arg ala ala pro arg pro ser asp ala asp ser ala ala ser arg cys asp gly trp
 1141/381
 cgc tcg gag cac gga cat cga gaa ctc tcg ggg ttc ggc gaa cgt tat ctc agt gga atc
 arg ser glu his gly his arg glu leu ser gly phe gly glu arg tyr leu ser gly ile
 1201/401
 tca gtc cac gcg cgc aac cta gtt gtg cag tta ctg ttg aaa gcc aca ccc atg cca gtc
 ser val his ala arg asn leu val val gln leu leu leu lys ala thr pro met pro val
 1261/421
 cac gca tgg cca agt tgg ccc gag tag tgg gcc tag tac agg aag agc aac cta gcg aca
 his ala trp pro ser trp pro glu AMB trp ala AMB tyr arg lys ser asn leu ala thr
 1321/441
 tga cga atc acc cac ggt att cgc cac cgc cgc agc agc cgg gaa ccc cag gtt atg ctc
 OPA arg ile thr his gly ile arg his arg arg ser ser arg glu pro gln val met leu
 1381/461
 agg ggc agc agc aaa cgt aca gcc agc agt tcg act ggc gtt acc cac cgt ccc cgc ccc
 arg gly ser ser lys arg thr ala ser ser ser thr gly val thr his arg pro arg pro
 1441/481
 cgc agc caa ccc agt acc gtc aac cct acg agg cgt tgg gtg gta ccc ggc cgg gtc tga
 arg ser gln pro ser thr val asn pro thr arg arg trp val val pro gly arg val OPA
 1501/501
 tac ctg gcg tga ttc cga cca tga cgc ccc ctc ctg gga tgg ttc gcc aac gcc ctc gtg
 tyr leu ala OPA phe arg pro OPA arg pro leu leu gly trp phe ala asn ala leu val
 1561/521
 cag gca tgt tgg cca tcg gcg cgg tga cga tag cgg tgg tgt ccg ccg gca tcg gcg gcg
 gln ala cys trp pro ser ala arg OPA arg AMB arg trp cys pro pro ala ser ala ala
 1621/541
 cgg ccg cat ccc tgg tcg ggt tca acc ggg cac ccg ccg gcc cca gcg gcg gcc cag tgg
 arg pro his pro trp ser gly ser thr gly his pro pro ala pro ala ala ala gln trp
 1681/561
 ctg cca gcg cgg cgc caa gca tcc ccg cag caa aca tgc cgc cgg ggt cgg tcg aac agg
 leu pro ala arg arg gln ala ser pro gln gln thr cys arg arg gly arg ser asn arg
 1741/581
 tgg cgg cca agg tgg tgc cca gtg tcg tca tgt tgg aaa ccg atc tgg gcc gcc agt cgg
 trp arg pro arg trp cys pro val ser ser cys trp lys pro ile trp ala ala ser arg
 1801/601
 agg agg gct ccg gca tca ttc tgt ctg ccg agg ggc tga tct tga cca aca acc acg tga
 arg arg ala pro ala ser phe cys leu pro arg gly OPA ser OPA pro thr thr thr OPA
 1861/621
 tcg cgg cgg ccg cca agc ctc ccc tgg gca gtc cgc cgc cga aaa cga cgg ta
 ser arg arg pro pro ser leu pro trp ala val arg arg arg lys arg arg

SEQ ID No.49B (continued 1)

FIGURE 49B (continued 1)

1/1
 atc tac acc gct caa cag ccg ggc cag acg ctg ccg gtc ggt gct gcc gag aag gcg gtg
 ile tyr thr ala gln gln pro gly gln thr leu pro val gly ala ala glu lys ala val
 61/21
 atc cgt ggc gag ttg ttc atg tcg cgg cgc acc acc gcc gac caa cgg gtg ctt gcc atc
 ile arg gly glu leu phe met ser arg arg thr thr ala asp gln arg val leu ala ile
 121/41
 cgt ctg acc aac ggt agt tcg ctg ctg atc tcc aaa agt ctc aag ccc acc gaa gca gtc
 arg leu thr asn gly ser ser leu leu ile ser lys ser leu lys pro thr glu ala val
 181/61
 atg aac aag ctg cgt tgg gtg cta ttg atc gtg ggt ggg atc ggg gtg gcg gtc gcc gcg
 met asn lys leu arg trp val leu leu ile val gly gly ile gly val ala val ala ala
 241/81
 gtg gcc ggg ggg atg gtc acc cgg gcc ggg ctg agg ccg gtg ggc cgc ctc acc gaa gcg
 val ala gly gly met val thr arg ala gly leu arg pro val gly arg leu thr glu ala
 301/101
 gcc gag cgg gtg gcg cga acc gac gac ctg cgg ccc atc ccc gtc ttc ggc agc gac gaa
 ala glu arg val ala arg thr asp asp leu arg pro ile pro val phe gly ser asp glu
 361/121
 ttg gcc agg ctg aca gag gca ttc aat tta atg ctg cgg gcg ctg gcc gag tca cgg gaa
 leu ala arg leu thr glu ala phe asn leu met leu arg ala leu ala glu ser arg glu
 421/141
 cgg cag gca agg ctg gtt acc gac gcc gga cat gaa ttg cgt acc ccg cta acg tcg ctg
 arg gln ala arg leu val thr asp ala gly his glu leu arg thr pro leu thr ser leu
 481/161
 cgc acc aat gtc gaa ctc ttg atg gcc tcg atg gcc ccg ggg gct ccg cgg cta ccc aag
 arg thr asn val glu leu leu met ala ser met ala pro gly ala pro arg leu pro lys
 541/181
 cag gag atg gtc gac ctg cgt gcc gat gtg ctg gct caa atc gag gaa ttg tcc aca ctg
 gln glu met val asp leu arg ala asp val leu ala gln ile glu glu leu ser thr leu
 601/201
 gta ggc gat ttg gtg gac ctg tcc cga ggc gac gcc gga gaa gtg gtg cac gag ccg gtc
 val gly asp leu val asp leu ser arg gly asp ala gly glu val val his glu pro val
 661/221
 gac atg gct gac gtc gtc gac cgc agc ctg gag cgg gtc agg cgg cgg cgc aac gat atc
 asp met ala asp val val asp arg ser leu glu arg val arg arg arg arg asn asp ile
 721/241
 ctt ttc gac gtc gag gtg att ggg tgg cag gtt tat ggc gat acc gct gga ttg tcg cgg
 leu phe asp val glu val ile gly trp gln val tyr gly asp thr ala gly leu ser arg
 781/261
 atg gcg ctt aac ctg atg gac aac gcc gcg aag tgg agc ccg ccg ggc ggc cac gtg ggt
 met ala leu asn leu met asp asn ala ala lys trp ser pro pro gly gly his val gly
 841/281
 gtc agg ctg agc cag ctc gac gcg tcg cac gct gag ctg gtg gtt tcc gac cgc ggc ccg
 val arg leu ser gln leu asp ala ser his ala glu leu val val ser asp arg gly pro
 901/301
 ggc att ccc gtg cag gag cgc cgt ctg gtg ttt gaa cgg ttt tac cgg tcg gca tcg gca
 gly ile pro val gln glu arg arg leu val phe glu arg phe tyr arg ser ala ser ala
 961/321
 cgg gcg ttg ccg ggt tcg ggc ctc ggg ttg gcg atc gtc aaa cag gtg gtg ctc aac cac
 arg ala leu pro gly ser gly leu gly leu ala ile val lys gln val val leu asn his

SEQ ID No.49C

FIGURE 49C

1021/341 ggc gga ttg ctg cgc atc gaa gac acc gac cca ggc ggc cag ccc cct gga acg tcg att
 gly gly leu leu arg ile glu asp thr asp pro gly gly gln pro pro gly thr ser ile
 1081/361 1111/371
 tac gtg ctg ctc ccc ggc cgt cgg atg ccg att ccg cag ctt ccc ggt gcg acg gct ggc
 tyr val leu leu pro gly arg arg met pro ile pro gln leu pro gly ala thr ala gly
 1141/381 1171/391
 gct cgg agc acg gac atc gag aac tct cgg ggt tcg gcg aac gtt atc tca gtg gaa tct
 ala arg ser thr asp ile glu asn ser arg gly ser ala asn val ile ser val glu ser
 1201/401 1231/411
 cag tcc acg cgc gca acc tag ttg tgc agt tac tgt tga aag cca cac cca tgc cag tcc
 gln ser thr arg ala thr AMB leu cys ser tyr cys OPA lys pro his pro cys gln ser
 1261/421 1291/431
 acg cat ggc caa gtt ggc ccg agt agt ggg cct agt aca gga aga gca acc tag cga cat
 thr his gly gln val gly pro ser ser gly pro ser thr gly arg ala thr AMB arg his
 1321/441 1351/451
 gac gaa tca ccc acg gta ttc gcc acc gcc gca gca gcc ggg aac ccc agg tta tgc tca
 asp glu ser pro thr val phe ala thr ala ala ala ala gly asn pro arg leu cys ser
 1381/461 1411/471
 ggg gca gca gca aac gta cag cca gca gtt cga ctg gcg tta ccc acc gtc ccc gcc ccc
 gly ala ala ala asn val gln pro ala val arg leu ala leu pro thr val pro ala pro
 1441/481 1471/491
 gca gcc aac cca gta ccg tca acc cta cga ggc gtt ggg tgg tac ccg gcc ggg tct gat
 ala ala asn pro val pro ser thr leu arg gly val gly trp tyr pro ala gly ser asp
 1501/501 1531/511
 acc tgg cgt gat tcc gac cat gac gcc ccc tcc tgg gat ggt tcg cca acg ccc tcg tgc
 thr trp arg asp ser asp his asp ala pro ser trp asp gly ser pro thr pro ser cys
 1561/521 1591/531
 agg cat gtt ggc cat cgg cgc ggt gac gat agc ggt ggt gtc cgc cgg cat cgg cgg cgc
 arg his val gly his arg arg gly asp asp ser gly gly val arg arg his arg arg arg
 1621/541 1651/551
 ggc cgc atc cct ggt cgg gtt caa ccg ggc acc cgc cgg ccc cag cgg cgg ccc agt ggc
 gly arg ile pro gly arg val gln pro gly thr arg arg pro gln arg arg pro ser gly
 1681/561 1711/571
 tgc cag cgc ggc gcc aag cat ccc cgc agc aaa cat gcc gcc ggg gtc ggt cga aca ggt
 cys gln arg gly ala lys his pro arg ser lys his ala ala gly val gly arg thr gly
 1741/581 1771/591
 ggc ggc caa ggt ggt gcc cag tgt cgt cat gtt gga aac cga tct ggg ccg cca gtc gga
 gly gly gln gly gly ala gln cys arg his val gly asn arg ser gly pro pro val gly
 1801/601 1831/611
 gga ggg ctc cgg cat cat tct gtc tgc cga ggg gct gat ctt gac caa caa cca cgt gat
 gly gly leu arg his his ser val cys arg gly ala asp leu asp gln gln pro arg asp
 1861/621 1891/631
 cgc ggc ggc cgc caa gcc tcc cct ggg cag tcc gcc gcc gaa aac gac ggt a
 arg gly gly arg gln ala ser pro gly gln ser ala ala glu asn asp gly

SEQ ID No.49C (continued 1)

FIGURE 49C (continued 1)

Coding sequence Rv0983 predicted by Cole et al., 1998 (Nature 393:537-544) and containing seq60A:

1/1	31/11
atg gcc aag ttg gcc cga gta gtg ggc cta	gta cag gaa gag caa cct agc gac atg acg
Met ala lys leu ala arg val val gly leu	val gln glu glu gln pro ser asp met thr
61/21	91/31
aat cac cca cgg tat tcg cca ccg ccg cag	cag ccg gga acc cca ggt tat gct cag ggg
asn his pro arg tyr ser pro pro pro gln	gln pro gly thr pro gly tyr ala gln gly
121/41	151/51
cag cag caa acg tac agc cag cag ttc gac	tgg cgt tac cca ccg tcc ccg ccc ccg cag
gln gln gln thr tyr ser gln gln phe asp	trp arg tyr pro pro ser pro pro pro gln
181/61	211/71
cca acc cag tac cgt caa ccc tac gag gcg	ttg ggt ggt acc ccg ccg ggt ctg ata cct
pro thr gln tyr arg gln pro tyr glu ala	leu gly gly thr arg pro gly leu ile pro
241/81	271/91
ggc gtg att ccg acc atg acg ccc cct cct	ggg atg gtt cgc caa cgc cct cgt gca ggc
gly val ile pro thr met thr pro pro pro	gly met val arg gln arg pro arg ala gly
301/101	331/111
atg ttg gcc atc ggc gcg gtg acg ata gcg	gtg gtg tcc gcc ggc atc ggc ggc gcg gcc
met leu ala ile gly ala val thr ile ala	val val ser ala gly ile gly gly ala ala
361/121	391/131
gca tcc ctg gtc ggg ttc aac ccg gca ccc	gcc gcc ccc agc ggc ggc cca gtg gct gcc
ala ser leu val gly phe asn arg ala pro	ala gly pro ser gly gly pro val ala ala
421/141	451/151
agc gcg gcg cca agc atc ccc gca gca aac	atg ccg ccg ggc tgc gtc gaa cag gtg gcg
ser ala ala pro ser ile pro ala ala asn	met pro pro gly ser val glu gln val ala
481/161	511/171
gcc aag gtg gtg ccc agt gtc gtc atg ttg	gaa acc gat ctg ggc cgc cag tgc gag gag
ala lys val val pro ser val val met leu	glu thr asp leu gly arg gln ser glu glu
541/181	571/191
ggc tcc ggc atc att ctg tct gcc gag ggg	ctg atc ttg acc aac aac cac gtg atc gcg
gly ser gly ile ile leu ser ala glu gly	leu ile leu thr asn asn his val ile ala
601/201	631/211
gcg gcc gcc aag cct ccc ctg ggc agt ccg	ccg ccg aaa acg acg gta acc ttc tct gac
ala ala ala lys pro pro leu gly ser pro	pro pro lys thr thr val thr phe ser asp
661/221	691/231
ggg ccg acc gca ccc ttc acg gtg gtg ggg	gct gac ccc acc agt gat atc gcc gtc gtc
gly arg thr ala pro phe thr val val gly	ala asp pro thr ser asp ile ala val val
721/241	751/251
cgt gtt cag ggc gtc tcc ggg ctc acc ccg	atc tcc ctg ggt tcc tcc tgc gac ctg agg
arg val gln gly val ser gly leu thr pro	ile ser leu gly ser ser ser asp leu arg
781/261	811/271
gtc ggt cag ccg gtg ctg gcg atc ggg tgc	ccg ctc ggt ttg gag ggc acc gtg acc acg
val gly gln pro val leu ala ile gly ser	pro leu gly leu glu gly thr val thr thr

SEQ ID No.49D

FIGURE 49D

841/281
 ggg atc gtc agc gct ctc aac cgt cca gtg tgc acg acc ggc gag gcc ggc aac cag aac
 gly ile val ser ala leu asn arg pro val ser thr thr gly glu ala gly asn gln asn
 901/301
 acc gtg ctg gac gcc att cag acc gac gcc gcg atc aac ccc ggt aac tcc ggg ggc gcg
 thr val leu asp ala ile gln thr asp ala ala ile asn pro gly asn ser gly gly ala
 961/321
 ctg gtg aac atg aac gct caa ctc gtc gga gtc aac tgc gcc att gcc acg ctg ggc gcg
 leu val asn met asn ala gln leu val gly val asn ser ala ile ala thr leu gly ala
 1021/341
 gac tca gcc gat gcg cag agc ggc tgc atc ggt ctc ggt ttt gcg att cca gtc gac cag
 asp ser ala asp ala gln ser gly ser ile gly leu gly phe ala ile pro val asp gln
 1081/361
 gcc aag cgc atc gcc gac gag ttg atc agc acc ggc aag gcg tca cat gcc tcc ctg ggt
 ala lys arg ile ala asp glu leu ile ser thr gly lys ala ser his ala ser leu gly
 1141/381
 gtg cag gtg acc aat gac aaa gac acc ctg ggc gcc aag atc gtc gaa gta gtg gcc ggt
 val gln val thr asn asp lys asp thr leu gly ala lys ile val glu val val ala gly
 1201/401
 ggt gct gcc gcg aac gct gga gtg ccg aag ggc gtc gtt gtc acc aag gtc gac gac cgc
 gly ala ala ala asn ala gly val pro lys gly val val val thr lys val asp asp arg
 1261/421
 ccg atc aac agc gcg gac gcg ttg gtt gcc gcc gtg ccg tcc aaa gcg ccg ggc gcc acg
 pro ile asn ser ala asp ala leu val ala ala val arg ser lys ala pro gly ala thr
 1321/441
 gtg gcg cta acc ttt cag gat ccc tgc ggc ggt agc cgc aca gtg caa gtc acc ctc ggc
 val ala leu thr phe gln asp pro ser gly gly ser arg thr val gln val thr leu gly
 1381/461
 aag gcg gag cag tga
 lys ala glu gln OPA

871/291

931/311

991/331

1051/351

1111/371

1171/391

1231/411

1291/431

1351/451

SEQ ID No.49D (continued 1)

FIGURE 49D (continued 1)

ORF according to Cole et al., 1998 (Nature 393:537-544) and containing Rv0983

1/1	31/11
tga gcc agc tcg acg cgt cgc acg ctg agc	tgg tgg ttt ccg acc gcg gcc cgg gca ttc
OPA ala ser ser thr arg arg thr leu ser	trp trp phe pro thr ala ala arg ala phe
61/21	91/31
ccg tgc agg agc gcc gtc tgg tgt ttg aac	ggt ttt acc ggt cgg cat cgg cac ggg cgt
pro cys arg ser ala val trp cys leu asn	gly phe thr gly arg his arg his gly arg
121/41	151/51
tgc cgg gtt cgg gcc tcg ggt tgg cga tcg	tca aac agg tgg tgc tca acc acg gcg gat
cys arg val arg ala ser gly trp arg ser	ser asn arg trp cys ser thr thr ala asp
181/61	211/71
tgc tgc gca tcg aag aca ccg acc cag gcg	gcc agc ccc ctg gaa cgt cga ttt acg tgc
cys cys ala ser lys thr pro thr gln ala	ala ser pro leu glu arg arg phe thr cys
241/81	271/91
tgc tcc ccg gcc gtc gga tgc cga ttc cgc	agc ttc ccg gtg cga cgg ctg gcg ctc gga
cys ser pro ala val gly cys arg phe arg	ser phe pro val arg arg leu ala leu gly
301/101	331/111
gca cgg aca tcg aga act ctc ggg gtt cgg	cga acg tta tct cag tgg aat ctc agt cca
ala arg thr ser arg thr leu gly val arg	arg thr leu ser gln trp asn leu ser pro
361/121	391/131
cgc gcg caa cct agt tgt gca gtt act gtt	gaa agc cac acc cat gcc agt cca cgc atg
arg ala gln pro ser cys ala val thr val	glu ser his thr his ala ser pro arg met
421/141	451/151
gcc aag ttg gcc cga gta gtg ggc cta gta	cag gaa gag caa cct agc gac atg acg aat
ala lys leu ala arg val val gly leu val	gln glu glu gln pro ser asp met thr asn
481/161	511/171
cac cca cgg tat tcg cca ccg ccg cag cag	ccg gga acc cca ggt tat gct cag ggg cag
his pro arg tyr ser pro pro pro gln gln	pro gly thr pro gly tyr ala gln gly gln
541/181	571/191
cag caa acg tac agc cag cag ttc gac tgg	cgt tac cca ccg tcc ccg ccc ccg cag cca
gln gln thr tyr ser gln gln phe asp trp	arg tyr pro pro ser pro pro pro gln pro
601/201	631/211
acc cag tac cgt caa ccc tac gag gcg ttg	ggt ggt acc cgg ccg ggt ctg ata cct ggc
thr gln tyr arg gln pro tyr glu ala leu	gly gly thr arg pro gly leu ile pro gly
661/221	691/231
gtg att ccg acc atg acg ccc cct cct ggg	atg gtt cgc caa cgc cct cgt gca ggc atg
val ile pro thr met thr pro pro pro gly	met val arg gln arg pro arg ala gly met
721/241	751/251
ttg gcc atc ggc gcg gtg acg ata gcg gtg	gtg tcc gcc ggc atc ggc ggc gcg gcc gca
leu ala ile gly ala val thr ile ala val	val ser ala gly ile gly gly ala ala ala
781/261	811/271
tcc ctg gtc ggg ttc aac ccg gca ccc gcc	ggc ccc agc ggc ggc cca gtg gct gcc agc
ser leu val gly phe asn arg ala pro ala	gly pro ser gly gly pro val ala ala ser
841/281	871/291
gcg gcg cca agc atc ccc gca gca aac atg	ccg ccg ggg tcg gtc gaa cag gtg gcg gcc
ala ala pro ser ile pro ala ala asn met	pro pro gly ser val glu gln val ala ala

SEQ ID No.49F

FIGURE 49F

901/301
 aag gtg gtg ccc agt gtc gtc atg ttg gaa acc gat ctg ggc cgc cag tcg gag gag ggc
 lys val val pro ser val val met leu glu thr asp leu gly arg gln ser glu glu gly
 961/321
 tcc ggc atc att ctg tct gcc gag ggg ctg atc ttg acc aac aac cac gtg atc gcg gcg
 ser gly ile ile leu ser ala glu gly leu ile leu thr asn asn his val ile ala ala
 1021/341
 gcc gcc aag cct ccc ctg ggc agt ccg ccg ccg aaa acg acg gta acc ttc tct gac ggg
 ala ala lys pro pro leu gly ser pro pro pro lys thr thr val thr phe ser asp gly
 1081/361
 cgg acc gca ccc ttc acg gtg gtg ggg gct gac ccc acc agt gat atc gcc gtc gtc cgt
 arg thr ala pro phe thr val val gly ala asp pro thr ser asp ile ala val val arg
 1141/381
 gtt cag ggc gtc tcc ggg ctc acc ccg atc tcc ctg ggt tcc tcc tcg gac ctg agg gtc
 val gln gly val ser gly leu thr pro ile ser leu gly ser ser ser asp leu arg val
 1201/401
 ggt cag ccg gtg ctg gcg atc ggg tcg ccg ctc ggt ttg gag ggc acc gtg acc acg ggg
 gly gln pro val leu ala ile gly ser pro leu gly leu glu gly thr val thr thr gly
 1261/421
 atc gtc agc gct ctc aac cgt cca gtg tcg acg acc ggc gag gcc ggc aac cag aac acc
 ile val ser ala leu asn arg pro val ser thr thr gly glu ala gly asn gln asn thr
 1321/441
 gtg ctg gac gcc att cag acc gac gcc gcg atc aac ccc ggt aac tcc ggg ggc gcg ctg
 val leu asp ala ile gln thr asp ala ala ile asn pro gly asn ser gly gly ala leu
 1381/461
 gtg aac atg aac gct caa ctc gtc gga gtc aac tcg gcc att gcc acg ctg ggc gcg gac
 val asn met asn ala gln leu val gly val asn ser ala ile ala thr leu gly ala asp
 1441/481
 tca gcc gat gcg cag agc ggc tcg atc ggt ctc ggt ttt gcg att cca gtc gac cag gcc
 ser ala asp ala gln ser gly ser ile gly leu gly phe ala ile pro val asp gln ala
 1501/501
 aag cgc atc gcc gac gag ttg atc agc acc ggc aag gcg tca cat gcc tcc ctg ggt gtg
 lys arg ile ala asp glu leu ile ser thr gly lys ala ser his ala ser leu gly val
 1561/521
 cag gtg acc aat gac aaa gac acc ctg ggc gcc aag atc gtc gaa gta gtg gcc ggt ggt
 gln val thr asn asp lys asp thr leu gly ala lys ile val glu val val ala gly gly
 1621/541
 gct gcc gcg aac gct gga gtg ccg aag ggc gtc gtt gtc acc aag gtc gac gac cgc ccg
 ala ala ala asn ala gly val pro lys gly val val val thr lys val asp asp arg pro
 1681/561
 atc aac agc gcg gac gcg ttg gtt gcc gcc gtg cgg tcc aaa gcg ccg ggc gcc acg gtg
 ile asn ser ala asp ala leu val ala ala val arg ser lys ala pro gly ala thr val
 1741/581
 gcg cta acc ttt cag gat ccc tcg ggc ggt agc cgc aca gtg caa gtc acc ctc ggc aag
 ala leu thr phe gln asp pro ser gly gly ser arg thr val gln val thr leu gly lys
 1801/601
 gcg gag cag tga
 ala glu gln OPA

SEQ ID No.49F (continued 1)

FIGURE 49F (continued 1)

Fragment amplified by PCR based on the sequence similarities with a serine protease of the E.coli HtrA family (creation of an SnaBI site at the 3' end) and subcloned into the vector pJVEDa:

```

1/1                               31/11
gat ccg gcg ggg cgg gtg tcg gcg cag gcg tgg ctg gcg gtc acg gcg gtg cgg gcg gtg
asp pro ala gly arg val ser ala gln ala trp leu ala val thr ala val arg ala val
61/21                               91/31
ccg ccg ggc tgt ggg gcg ccg gcg gcg gcg gtg gca atg gcg gga acg gcg ccg atg cca
pro pro gly cys gly ala pro ala ala ala val ala met ala gly thr ala pro met pro
121/41                               151/51
aca tcg tca gcg gtg gag acg gtg gcc tcg gcg gtg ccg gtg gcg gtg gcg gat ggc tct
thr ser ser ala val glu thr val ala ser ala val pro val ala val ala asp gly ser
181/61                               211/71
acg gcg acg gcg ggg ccg gcg gac acg gcg gac aag gcg caa tcg gcc tcg gcg gcg gcg
thr ala thr ala gly pro ala asp thr ala asp lys ala gln ser ala ser ala ala ala
241/81                               271/91
ccg gcg gcg acg ggg gcc agg gcg gcg ccg gcc gcg gac tgt ggg gta ctg gcg gcg ccg
pro ala ala thr gly ala arg ala ala pro ala ala asp cys gly val leu ala ala pro
301/101                              331/111
gcg gac acg gcg ggc aag gcg gtg gta ccg ggg gcc cac cgc tgc ccg gtc agg cag gca
ala asp thr ala gly lys ala val val pro gly ala his arg cys pro val arg gln ala
361/121                              391/131
tgg gcg ccg cgg gtg gcg ccg gtg gcc tga tcg gca acg gcg ggg ccg gcg gcg acg gcg
trp ala pro arg val ala pro val gly OPA ser ala thr ala gly pro ala ala thr ala
421/141                              451/151
gtg tcg gcg cgt ccg gcg ggg tcg ccg gag tag gcg gtg ccg gcg gga acg cca tgc tga
val ser ala arg pro ala gly ser pro glu AMB ala val pro ala gly thr pro cys OPA
481/161                              511/171
tcg gcc acg gcg gcg ccg gcg gcg ccg gcg gag aca gca gtt tcg cta atg gcg ccg ccg
ser gly thr ala ala pro ala ala pro ala glu thr ala val ser leu met ala arg pro
541/181                              571/191
gcg gcg ccg gcg gtg ccg gag ggc acc tct tcg gca atg gcg ggt ccg gcg gcc acg gcg
ala ala arg ala val pro glu gly thr ser ser ala met ala gly pro ala ala thr ala
601/201                              631/211
gag ccg tca cgg ccg gca aca ccg gta tcg gtg gcg ccg gcg gcg tcg gtg ggg acg cca
glu pro ser arg pro ala thr pro val ser val ala pro ala ala ser val gly thr pro
661/221                              691/231
ggc tga tcg gcc acg gtg gcg ccg gcg gtg ccg gcg ggg acc gcg ccg gag cct tgg ttg
gly OPA ser ala thr val ala pro ala val pro ala gly thr ala pro glu pro trp leu
721/241                              751/251
gcc gtg acg gcg ggc ccg gtg gga acg ggg gcg ctg gcg gcc agc tat acg gca acg gcg
ala val thr ala gly pro val gly thr gly ala leu ala ala ser tyr thr ala thr ala
781/261                              811/271
gcg acg gcg ccc ccg gca ccg gcg gaa cac tgc agg ccg ccg tga gcg gat tgg tga ccg
ala thr ala pro pro ala pro ala glu his cys arg arg arg OPA ala asp trp OPA arg
841/281                              871/291
ctt tgt tcg gtg cac ccg gcc aac ccg gcg aca ccg gcc aac ccg gct agc ccc gat caa
leu cys ser val his pro ala asn pro ala thr pro ala asn pro ala ser pro asp gln
901/301                              931/311
cga ggg ttt cgg tgc cgg tcc ggg gca tgg cca tcc gct gag ctg gcg atc tgg act acg
arg gly phe arg cys arg ser gly ala trp pro ser ala glu leu ala ile trp thr thr
961/321                              991/331
ttg gtg tag aaa aat cct gcc gcc ccg acc ctt aag gct ggg aca att tct gat agc tac
leu val AMB lys asn pro ala ala arg thr leu lys ala gly thr ile ser asp ser tyr
1021/341                             1051/351
ccc gac aca gga ggt tac ggg atg agc aat tcg cgc cgc cgc tca ctc agg tgg tca tgg
pro asp thr gly gly tyr gly met ser asn ser arg arg arg ser leu arg trp ser trp
1081/361                             1111/371
ttg ctg agc gtg ctg gct gcc gtc ggg ctg ggc ctg gcc acg gcg ccg gcc cag gcg gcc
leu leu ser val leu ala ala val gly leu gly leu ala thr ala pro ala gln ala ala
1141/381
ccg ccg gcc ttg tcg cag gac ccg tt
pro pro ala leu ser gln asp arg

```

SEQ ID No.50A

FIGURE 50A

REPLACEMENT SHEET (RULE 26)

1/1
 atc cgg cgg ggc ggg tgt cgg cgc agg cgt ggc tgg cgg tca cgg cgg tgc ggg cgg tgc
 ile arg arg gly gly cys arg arg arg arg gly trp arg ser arg arg cys gly arg cys
 61/21
 cgc cgg gct gtg ggg cgc cgg cgg cgg cgg tgg caa tgg cgg gaa cgg cgc cga tgc caa
 arg arg ala val gly arg arg arg arg trp gln trp arg glu arg arg arg cys gln
 121/41
 cat cgt cag cgg tgg aga cgg tgg cct cgg cgg tgc cgg tgg cgg tgg cgg atg gct cta
 his arg gln arg trp arg arg trp pro arg arg cys arg trp arg trp arg met ala leu
 181/61
 cgg cga cgg cgg ggc cgg cgg aca cgg cgg aca agg cgc aat cgg cct cgg cgg cgg cgc
 arg arg arg arg gly arg arg thr arg arg thr arg arg asn arg pro arg arg arg arg
 241/81
 cgg cgg cga cgg ggg cca ggg cgg cgc cgg cgg cgg act gtg ggg tac tgg cgg cgc cgg
 arg arg arg arg gly pro gly arg arg arg pro arg thr val gly tyr trp arg arg arg
 301/101
 cgg aca cgg cgg gca agg cgg tgg tac cgg ggg ccc acc gct gcc cgg tca ggc agg cat
 arg thr arg arg ala arg arg trp tyr arg gly pro thr ala ala arg ser gly arg his
 361/121
 ggg cgc cgc ggg tgg cgc cgg tgg gct gat cgg caa cgg cgg ggc cgg cgg cga cgg cgg
 gly arg arg gly trp arg arg trp ala asp arg gln arg arg gly arg arg arg arg arg
 421/141
 tgt cgg cgc gtc cgg cgg ggt cgc cgg agt agg cgg tgc cgg cgg gaa cgc cat gct gat
 cys arg arg val arg arg gly arg arg ser arg arg cys arg arg glu arg his ala asp
 481/161
 cgg gca cgg cgg cgc cgg cgg cgc cgg cgg aga cag cag ttt cgc taa tgg cgc ggc cgg
 arg ala arg arg arg arg arg arg arg arg arg gln gln phe arg OCH trp arg gly arg
 541/181
 cgg cgc ggg cgg tgc cgg agg gca cct ctt cgg caa tgg cgg gtc cgg cgg cca cgg cgg
 arg arg gly arg cys arg arg ala pro leu arg gln trp arg val arg arg pro arg arg
 601/201
 agc cgt cac ggc cgg caa cac cgg tat cgg tgg cgc cgg cgg cgt cgg tgg gga cgc cag
 ser arg his gly arg gln his arg tyr arg trp arg arg arg arg arg trp gly arg gln
 661/221
 gct gat cgg cca cgg tgg cgc cgg cgg tgc cgg cgg gga ccg cgc cgg agc ctt ggt tgg
 ala asp arg pro arg trp arg arg arg cys arg arg gly pro arg arg ser leu gly trp
 721/241
 ccg tga cgg cgg gcc cgg tgg gaa cgg ggg cgc tgg cgg cca gct ata cgg caa cgg cgg
 pro OPA arg arg ala arg trp glu arg gly arg trp arg pro ala ile arg gln arg arg
 781/261
 cga cgg cgc ccc cgg cac cgg cgg aac act gca ggc ggc ggt gag cgg att ggt gac ggc
 arg arg arg pro arg his arg arg asn thr ala gly gly gly glu arg ile gly asp gly
 841/281
 ttt gtt cgg tgc acc cgg cca acc cgg cga cac cgg cca acc cgg cta gcc ccg atc aac
 phe val arg cys thr arg pro thr arg arg his arg pro thr arg leu ala pro ile asn
 901/301
 gag ggt ttc ggt gcc ggt ccg ggg cat ggc cat ccg ctg agc tgg cga tct gga cta cgt
 glu gly phe gly ala gly pro gly his gly his pro leu ser trp arg ser gly leu arg
 961/321
 tgg tgt aga aaa atc ctg ccg ccc gga ccc tta agg ctg gga caa ttt ctg ata gct acc
 trp cys arg lys ile leu pro pro gly pro leu arg leu gly gln phe leu ile ala thr
 1021/341
 ccg aca cag gag gtt acg gga tga gca att cgc gcc gcc gct cac tca ggt ggt cat ggt
 pro thr gln glu val thr gly OPA ala ile arg ala ala ala his ser gly gly his gly
 1081/361
 tgc tga cgc tgc tgg ctg ccg tgc ggc tgg gcc tgg cca cgg cgc cgg ccc agg cgg ccc
 cys OPA ala cys trp leu pro ser gly trp ala trp pro arg arg arg pro arg arg pro
 1141/381
 cgc cgg cct tgt cgc agg acc ggt t
 arg arg pro cys arg arg thr gly

SEQ ID No.50B

FIGURE 50B

1/1
 tcc ggc ggc gcg ggt gtc ggc gca ggc gtg gct ggc ggt cac ggc ggt gcg ggc ggt gcc
 ser gly gly ala gly val gly ala gly val ala gly gly his gly gly ala gly gly ala
 61/21
 gcc ggc ctg tgg ggc gcc ggc ggc ggc ggt ggc aat ggc ggc aac ggc gcc gat gcc aac
 ala gly leu trp gly ala gly gly gly gly gly asn gly gly asn gly ala asp ala asn
 121/41
 atc gtc agc ggt gga gac ggt ggc ctc ggc ggt gcc ggt ggc ggt ggc gga tgg ctc tac
 ile val ser gly gly asp gly gly leu gly gly ala gly gly gly gly gly gly trp leu tyr
 181/61
 ggc gac ggc ggc gcc ggc gga cac ggc gga caa ggc gca atc ggc ctc ggc ggc ggc gcc
 gly asp gly gly ala gly gly his gly gly gln gly ala ile gly leu gly gly gly ala
 241/81
 ggc ggc gac ggc ggc cag ggc ggc gcc ggc cgc gga ctg tgg ggt act ggc ggc gcc ggc
 gly gly asp gly gly gln gly gly ala gly arg gly leu trp gly thr gly gly ala gly
 301/101
 gga cac ggc ggc caa ggc ggt ggt acc ggc ggc cca ccg ctg ccc ggt cag gca ggc atg
 gly his gly gly gln gly gly gly thr gly gly pro pro leu pro gly gln ala gly met
 361/121
 ggc gcc gcg ggt ggc gcc ggt ggc ctg atc ggc aac ggc ggc gcc ggc ggc gac ggc ggt
 gly ala ala gly gly ala gly gly leu ile gly asn gly gly ala gly gly asp gly gly
 421/141
 gtc ggc gcg tcc ggc ggc gtc gcc gga gta ggc ggt gcc ggc ggc aac gcc atg ctg atc
 val gly ala ser gly gly val ala gly val gly gly ala gly gly asn ala met leu ile
 481/161
 ggc cac ggc ggc gcc ggc ggc gcc ggc gga gac agc agt ttc gct aat ggc gcg gcc ggc
 gly his gly gly ala gly gly ala gly gly asp ser ser phe ala asn gly ala ala gly
 541/181
 ggc gcg ggc ggt gcc gga ggc cac ctc ttc ggc aat ggc ggc tcc ggc ggc cac ggc gga
 gly ala gly gly ala gly gly his leu phe gly asn gly gly ser gly gly his gly gly
 601/201
 gcc gtc acg gcc ggc aac acc ggt atc ggt ggc gcc ggc ggc gtc ggt ggc gac gcc agg
 ala val thr ala gly asn thr gly ile gly gly ala gly gly val gly gly asp ala arg
 661/221
 ctg atc ggc cac ggt ggc gcc ggc ggt gcc ggc ggc gac gcg gcc gga gcc ttg gtt ggc
 leu ile gly his gly gly ala gly gly ala gly gly asp arg ala gly ala leu val gly
 721/241
 cgt gac ggc ggc ccc ggt ggc aac ggc ggc gct ggc ggc cag cta tac ggc aac ggc ggc
 arg asp gly gly pro gly gly asn gly gly ala gly gly gln leu tyr gly asn gly gly
 781/261
 gac ggc gcc ccc ggc acc ggc gga aca ctg cag gcg gcg gtg agc gga ttg gtg acg gct
 asp gly ala pro gly thr gly gly thr leu gln ala ala val ser gly leu val thr ala
 841/281
 ttg ttc ggt gca ccc ggc caa ccc ggc gac acc ggc caa ccc ggc tag ccc cga tca acg
 leu phe gly ala pro gly gln pro gly asp thr gly gln pro gly AMB pro arg ser thr
 901/301
 agg gtt tcg gtg ccg gtc cgg ggc atg gcc atc cgc tga gct ggc gat ctg gac tac gtt
 arg val ser val pro val arg gly met ala ile arg OPA ala gly asp leu asp tyr val
 961/321
 ggt gta gaa aaa tcc tgc gcg ccg gac cct taa ggc tgg gac aat ttc tga tag cta ccc
 gly val glu lys ser cys arg pro asp pro OCH gly trp asp asn phe OPA AMB leu pro
 1021/341
 cga cac agg agg tta cgg gat gag caa ttc gcg ccg ccg ctc act cag gtg gtc atg gtt
 arg his arg arg leu arg asp glu gln phe ala pro pro leu thr gln val val met val
 1081/361
 gct gag cgt gct ggc tgc cgt cgg gct ggc cct ggc cac ggc gcc ggc cca ggc ggc ccc
 ala glu arg ala gly cys arg arg ala gly pro gly his gly ala gly pro gly gly pro
 1141/381
 gcc ggc ctt gtc gca gga ccg gtt
 ala gly leu val ala gly pro val

SEQ ID No.50C

FIGURE 50C

Coding sequence Rv0125 predicted by Cole et al., 1998 (Nature 393:537-544) and containing seq50A:

```

1/1                               31/11
atg agc aat tcg cgc cgc cgc tca ctc agg tgg tca tgg ttg ctg agc gtg ctg gct gcc
Met ser asn ser arg arg arg ser leu arg trp ser trp leu leu ser val leu ala ala
61/21                               91/31
gtc ggg ctg ggc ctg gcc acg gcg ccg gcc cag gcg gcc ccg ccg gcc ttg tcg cag gac
val gly leu gly leu ala thr ala pro ala gln ala ala pro pro ala leu ser gln asp
121/41                             151/51
cgg ttc gcc gac ttc ccc gcg ctg ccc ctc gac ccg tcc gcg atg gtc gcc caa gtg ggg
arg phe ala asp phe pro ala leu pro leu asp pro ser ala met val ala gln val gly
181/61                             211/71
cca cag gtg gtc aac atc aac acc aaa ctg ggc tac aac aac gcc gtg ggc gcc ggg acc
pro gln val val asn ile asn thr lys leu gly tyr asn asn ala val gly ala gly thr
241/81                             271/91
ggc atc gtc atc gat ccc aac ggt gtc gtg ctg acc aac aac cac gtg atc gcg ggc gcc
gly ile val ile asp pro asn gly val val leu thr asn asn his val ile ala gly ala
301/101                           331/111
acc gac atc aat gcg ttc agc gtc ggc tcc ggc caa acc tac ggc gtc gat gtg gtc ggg
thr asp ile asn ala phe ser val gly ser gly gln thr tyr gly val asp val val gly
361/121                           391/131
tat gac cgc acc cag gat gtc gcg gtg ctg cag ctg cgc ggt gcc ggt ggc ctg ccg tcg
tyr asp arg thr gln asp val ala val leu gln leu arg gly ala gly gly leu pro ser
421/141                           451/151
gcg gcg atc ggt ggc ggc gtc gcg gtt ggt gag ccc gtc gtc gcg atg ggc aac agc ggt
ala ala ile gly gly gly val ala val gly glu pro val val ala met gly asn ser gly
481/161                           511/171
ggg cag ggc gga acg ccc cgt gcg gtg cct ggc agg gtg gtc gcg ctc ggc caa acc gtg
gly gln gly gly thr pro arg ala val pro gly arg val val ala leu gly gln thr val
541/181                           571/191
cag gcg tcg gat tcg ctg acc ggt gcc gaa gag aca ttg aac ggg ttg atc cag ttc gat
gln ala ser asp ser leu thr gly ala glu glu thr leu asn gly leu ile gln phe asp
601/201                           631/211
gcc gcg atc cag ccc ggt gat tcg ggc ggg ccc gtc gtc aac ggc cta gga cag gtg gtc
ala ala ile gln pro gly asp ser gly gly pro val val asn gly leu gly gln val val
661/221                           691/231
ggt atg aac acg gcc gcg tcc gat aac ttc cag ctg tcc cag ggt ggg cag gga ttc gcc
gly met asn thr ala ala ser asp asn phe gln leu ser gln gly gly gln gly phe ala
721/241                           751/251
att ccg atc ggg cag gcg atg gcg atc gcg ggc cag atc cga tcg ggt ggg ggg tca ccc
ile pro ile gly gln ala met ala ile ala gly gln ile arg ser gly gly gly ser pro
781/261                           811/271
acc gtt cat atc ggg cct acc gcc ttc ctc ggc ttg ggt gtt gtc gac aac aac ggc aac
thr val his ile gly pro thr ala phe leu gly leu gly val val asp asn asn gly asn
841/281                           871/291
ggc gca cga gtc caa cgc gtg gtc ggg agc gct ccg gcg gca agt ctc ggc atc tcc acc
gly ala arg val gln arg val val gly ser ala pro ala ala ser leu gly ile ser thr
901/301                           931/311
ggc gac gtg atc acc gcg gtc gac ggc gct ccg atc aac tcg gcc acc gcg atg gcg gac
gly asp val ile thr ala val asp gly ala pro ile asn ser ala thr ala met ala asp
961/321                           991/331
gcg ctt aac ggg cat cat ccc ggt gac gtc atc tcg gtg acc tgg caa acc aag tcg ggc
ala leu asn gly his his pro gly asp val ile ser val thr trp gln thr lys ser gly
1021/341                          1051/351
ggc acg cgt aca ggg aac gtg aca ttg gcc gag gga ccc ccg gcc tga
gly thr arg thr gly asn val thr leu ala glu gly pro pro ala OPA

```

SEQ ID No.50D

FIGURE 50D

ORF according to Cole et al., 1998 (Nature 393:537-544) and containing Rv0125:

```

1/1                                31/11
tag aaa aat cct gcc gcc cgg acc ctt aag gct ggg aca att tct gat agc tac ccc gac
AMB lys asn pro ala ala arg thr leu lys ala gly thr ile ser asp ser tyr pro asp
61/21                                91/31
aca gga ggt tac ggg atg agc aat tcg cgc cgc cgc tca ctc agg tgg tca tgg ttg ctg
thr gly gly tyr gly met ser asn ser arg arg arg ser leu arg trp ser trp leu leu
121/41                                151/51
agc gtg ctg gct gcc gtc ggg ctg ggc ctg gcc acg gcg ccg gcc cag gcg gcc ccg ccg
ser val leu ala ala val gly leu gly leu ala thr ala pro ala gln ala ala pro pro
181/61                                211/71
gcc ttg tcg cag gac cgg ttc gcc gac ttc ccc gcg ctg ccc ctc gac ccg tcc gcg atg
ala leu ser gln asp arg phe ala asp phe pro ala leu pro leu asp pro ser ala met
241/81                                271/91
gtc gcc caa gtg ggg cca cag gtg gtc aac atc aac acc aaa ctg ggc tac aac aac gcc
val ala gln val gly pro gln val val asn ile asn thr lys leu gly tyr asn asn ala
301/101                                331/111
gtg ggc gcc ggg acc ggc atc gtc atc gat ccc aac ggt gtc gtg ctg acc aac aac cac
val gly ala gly thr gly ile val ile asp pro asn gly val val leu thr asn asn his
361/121                                391/131
gtg atc gcg ggc gcc acc gac atc aat gcg ttc agc gtc ggc tcc ggc caa acc tac ggc
val ile ala gly ala thr asp ile asn ala phe ser val gly ser gly gln thr tyr gly
421/141                                451/151
gtc gat gtg gtc ggg tat gac cgc acc cag gat gtc gcg gtg ctg cag ctg cgc ggt gcc
val asp val val gly tyr asp arg thr gln asp val ala val leu gln leu arg gly ala
481/161                                511/171
ggt ggc ctg ccg tcg gcg gcg atc ggt ggc ggc gtc gcg gtt ggt gag ccc gtc gtc gcg
gly gly leu pro ser ala ala ile gly gly gly val ala val gly glu pro val val ala
541/181                                571/191
atg ggc aac agc ggt ggg cag ggc gga acg ccc cgt gcg gtg cct ggc agg gtg gtc gcg
met gly asn ser gly gly gln gly gly thr pro arg ala val pro gly arg val val ala
601/201                                631/211
ctc ggc caa acc gtg cag gcg tcg gat tcg ctg acc ggt gcc gaa gag aca ttg aac ggg
leu gly gln thr val gln ala ser asp ser leu thr gly ala glu glu thr leu asn gly
661/221                                691/231
ttg atc cag ttc gat gcc gcg atc cag ccc ggt gat tcg ggc ggg ccc gtc gtc aac ggc
leu ile gln phe asp ala ala ile gln pro gly asp ser gly gly pro val val asn gly
721/241                                751/251
cta gga cag gtg gtc ggt atg aac acg gcc gcg tcc gat aac ttc cag ctg tcc cag ggt
leu gly gln val val gly met asn thr ala ala ser asp asn phe gln leu ser gln gly
781/261                                811/271
ggg cag gga ttc gcc att ccg atc ggg cag gcg atg gcg atc gcg ggc cag atc cga tcg
gly gln gly phe ala ile pro ile gly gln ala met ala ile ala gly gln ile arg ser
841/281                                871/291
ggt ggg ggg tca ccc acc gtt cat atc ggg cct acc gcc ttc ctc ggc ttg ggt gtt gtc
gly gly gly ser pro thr val his ile gly pro thr ala phe leu gly leu gly val val
901/301                                931/311
gac aac aac ggc aac ggc gca cga gtc caa cgc gtg gtc ggg agc gct ccg gcg gca agt
asp asn asn gly asn gly ala arg val gln arg val val gly ser ala pro ala ala ser
961/321                                991/331
ctc ggc atc tcc acc ggc gac gtg atc acc gcg gtc gac ggc gct ccg atc aac tcg gcc
leu gly ile ser thr gly asp val ile thr ala val asp gly ala pro ile asn ser ala
1021/341                                1051/351
acc gcg atg gcg gac gcg ctt aac ggg cat cat ccc ggt gac gtc atc tcg gtg acc tgg
thr ala met ala asp ala leu asn gly his his pro gly asp val ile ser val thr trp
1081/361                                1111/371
caa acc aag tcg ggc ggc acg cgt aca ggg aac gtg aca ttg gcc gag gga ccc ccg gcc
gln thr lys ser gly gly thr arg thr gly asn val thr leu ala glu gly pro pro ala
1141/381
tga
OPA

```

SEQ ID No.50F

FIGURE 50F

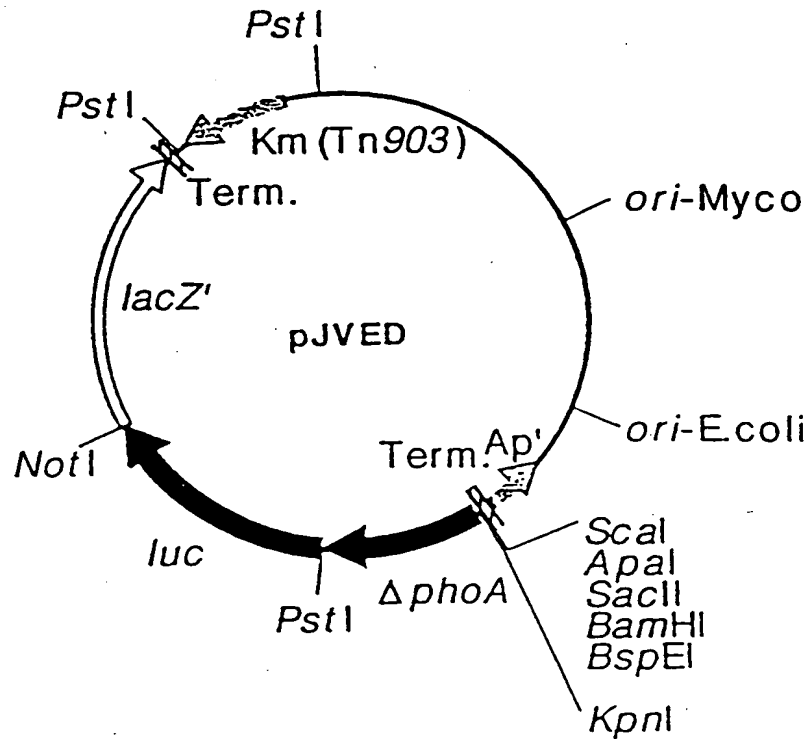


FIGURE 51A

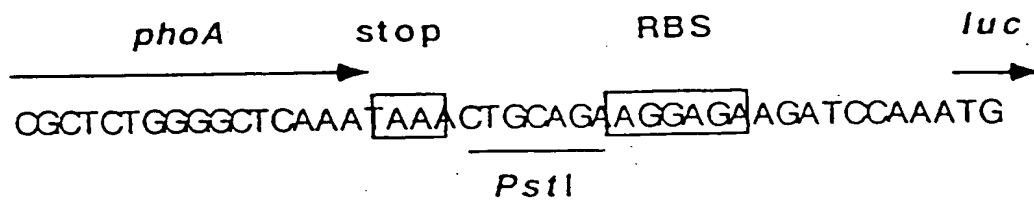


FIGURE 51B

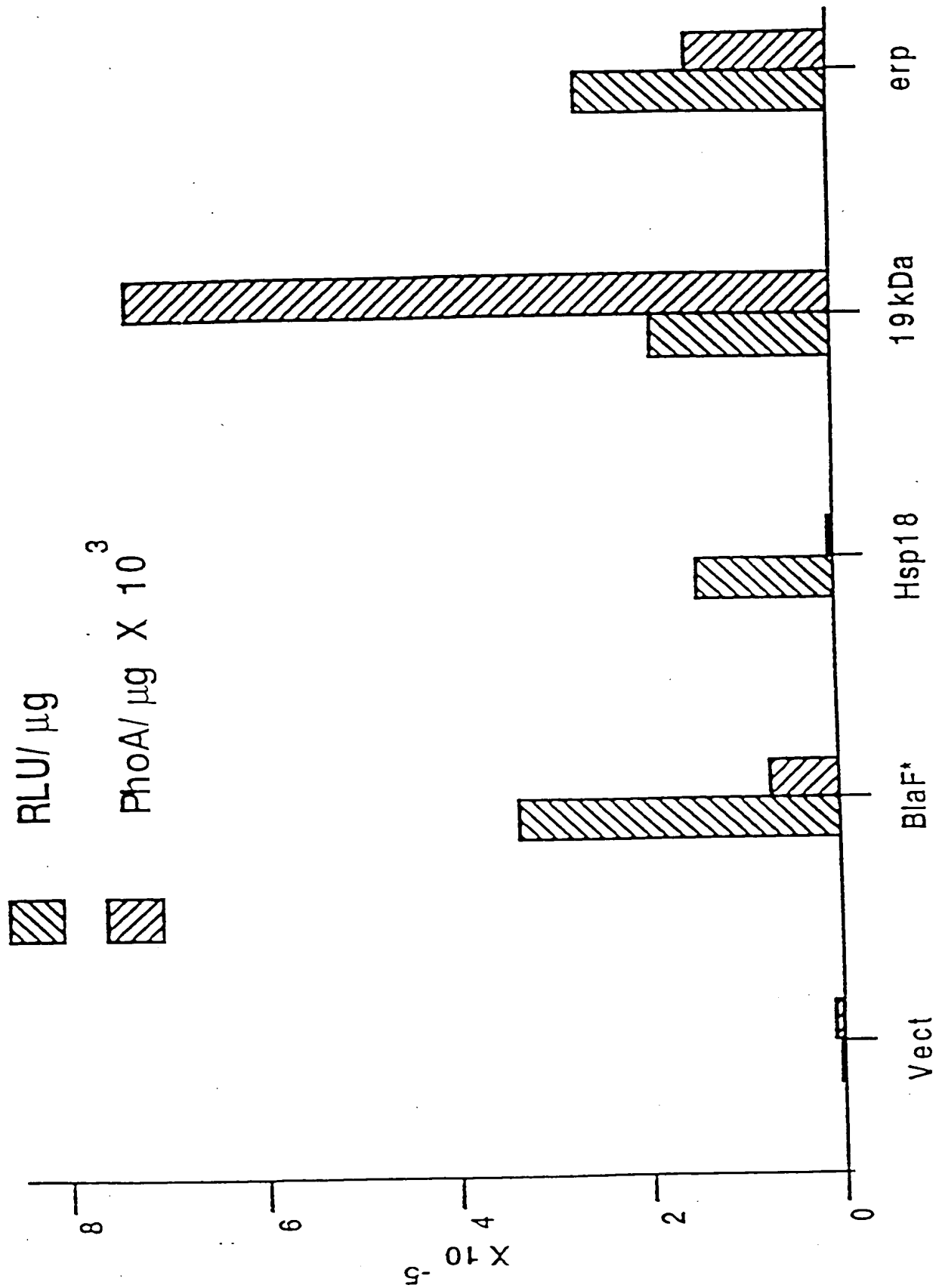


FIGURE 53

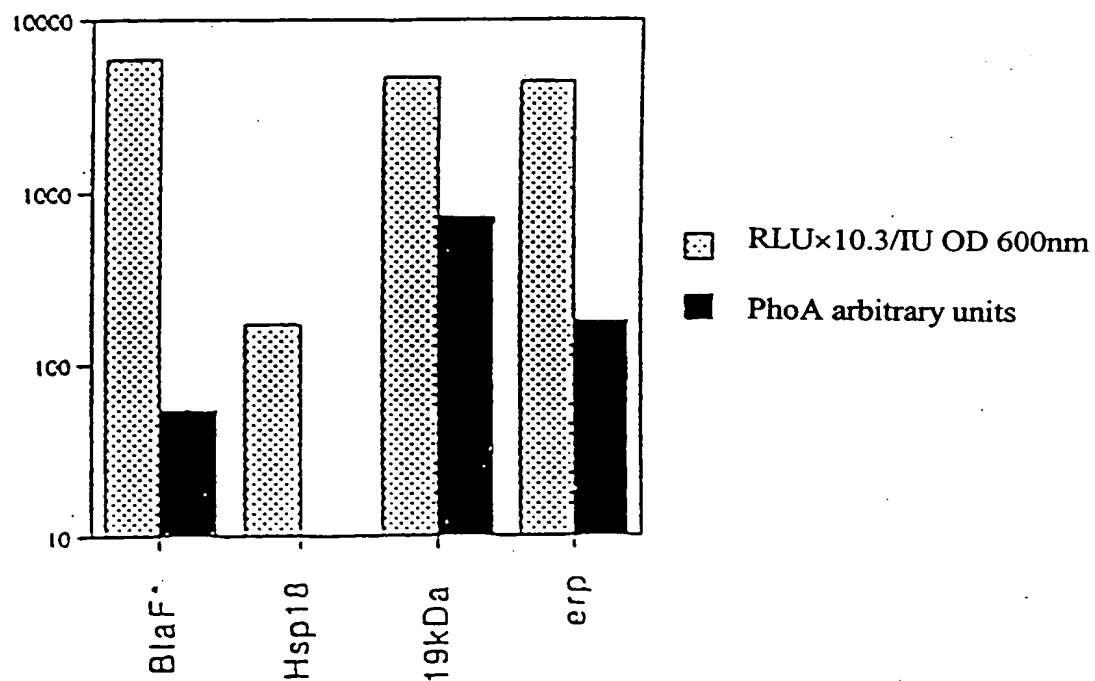


FIGURE 54

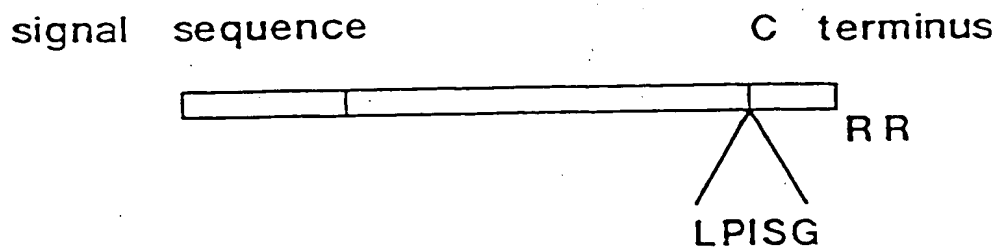
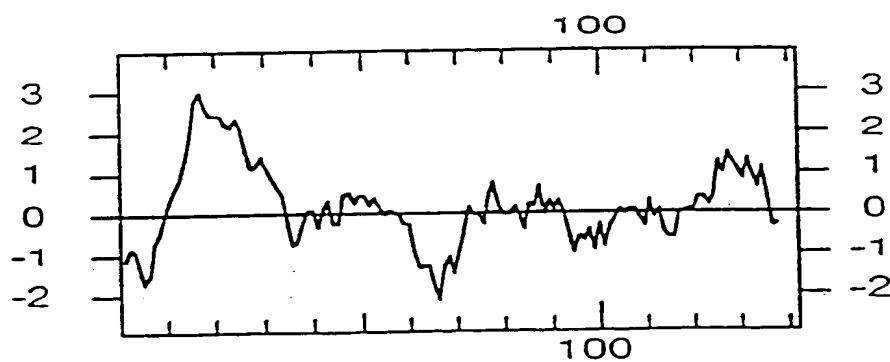


FIGURE 55

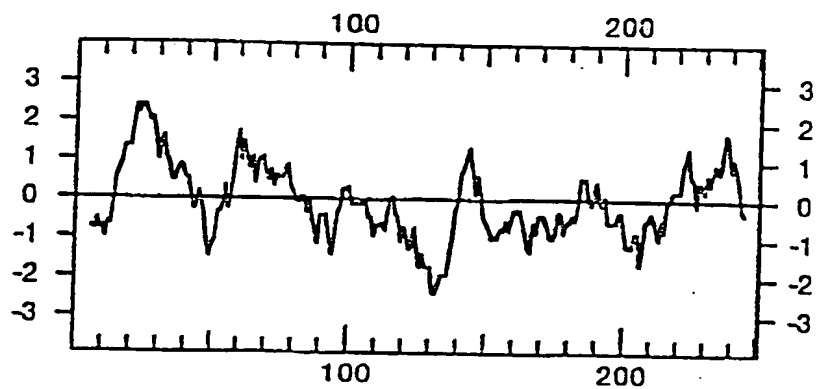


FIGURE 56

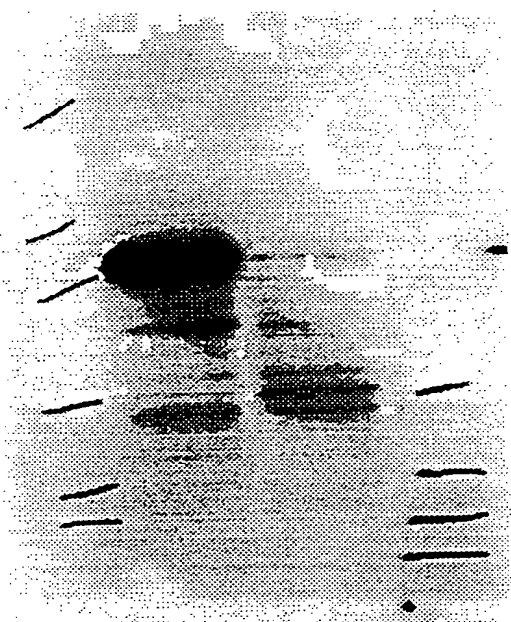


FIGURE 57A

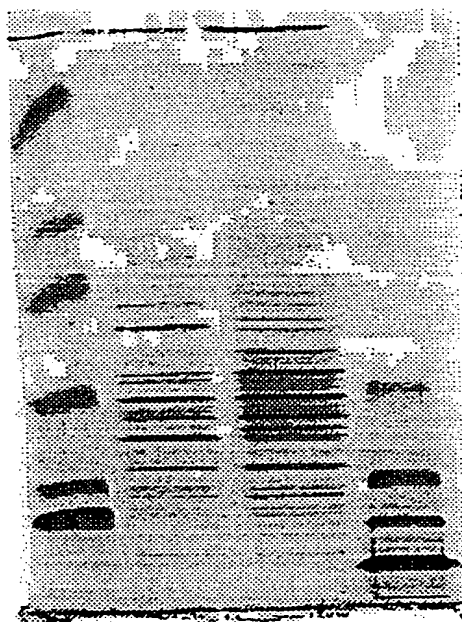


FIGURE 57B